

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds
(without alignments)
1684.164 Million cell updates/sec

Title: US-09-310-844c-25
Perfect score: 29
Sequence: 1 aaagaucuuuuuuuaagccccaagggcu 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rtd.*
- 36: em.htg.nam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	29	100.0	42	6	BD274272	BD274272 Identific
2	29	100.0	42	6	BD274273	BD274273 Identific
3	29	100.0	42	6	BD274280	BD274280 Identific
4	29	100.0	42	6	BD274281	BD274281 Identific
5	28	96.6	46	6	BD274241	BD274241 Identific
6	28	96.6	46	6	BD274242	BD274242 Identific
7	28	96.6	46	6	BD274243	BD274243 Identific
8	28	96.6	46	6	BD274258	BD274258 Identific
9	28	96.6	46	6	BD274259	BD274259 Identific
10	28	96.6	46	6	BD274260	BD274260 Identific
11	24.8	85.5	42	6	BD274270	BD274270 Identific
12	24.8	85.5	42	6	BD274278	BD274278 Identific
13	23.8	82.1	46	6	BD274238	BD274238 Identific
14	23.8	82.1	46	6	BD274256	BD274256 Identific
15	23.2	80.0	42	6	BD274275	BD274275 Identific
16	23.2	80.0	42	6	BD274283	BD274283 Identific
17	22.2	76.6	46	6	BD274240	BD274240 Identific
18	22.2	76.6	46	6	BD274249	BD274249 Identific
19	22.2	76.6	46	6	BD274252	BD274252 Identific
20	22.2	76.6	46	6	BD274253	BD274253 Identific
21	22.2	76.6	46	6	BD274257	BD274257 Identific
22	22.2	76.6	46	6	BD274265	BD274265 Identific
23	22.2	76.6	46	6	BD274268	BD274268 Identific
24	22.2	76.6	46	6	BD274269	BD274269 Identific
25	21.2	73.1	42	6	BD274271	BD274271 Identific
26	21.2	73.1	42	6	BD274279	BD274279 Identific
27	21.2	73.1	46	6	BD274247	BD274247 Identific
28	21.2	73.1	46	6	BD274263	BD274263 Identific
29	20	69.0	46	6	BD274237	BD274237 Identific
30	20	69.0	46	6	BD274251	BD274251 Identific
31	20	69.0	46	6	BD274255	BD274255 Identific
32	20	69.0	46	6	BD274277	BD274277 Identific
33	19.6	67.6	42	6	BD274284	BD274284 Identific
34	18.6	64.1	46	6	BD274246	BD274246 Identific
35	18.6	64.1	46	6	BD274248	BD274248 Identific
36	18.6	64.1	46	6	BD274262	BD274262 Identific
37	18.6	64.1	46	6	BD274264	BD274264 Identific
38	18.4	63.4	42	6	BD274274	BD274274 Identific
39	18.4	63.4	42	6	BD274282	BD274282 Identific
40	18.4	63.4	43	8	ATH553793	BD274277 Arabidops
41	18	62.1	44	6	BD274277	BD274277 Identific
C 42	16.4	56.6	31	6	AX425989	AX425989 Sequence
C 43	16.4	56.6	42	6	BD274276	BD274276 Identific
C 44	16.2	55.9	48	6	AX018731	AX018731 Sequence
C 45	16.2	55.9	79	6	AX914035	AX914035 Sequence
C 46	16.2	55.9	79	6	BD049568	BD049568 Sequence
C 47	15.4	53.1	73	6	E02131	E02131 Pseudoknot
C 48	15.2	52.4	33	6	AR020509	AR020509 Sequence
C 49	15.2	52.4	47	6	AR289362	AR289362 Sequence
50	15	51.7	23	6	E09974	E10118 PCR primer
51	15	51.7	23	6	E10118	E10118 PCR primer
52	15	51.7	30	6	AX793341	AX793341 Sequence
C 53	15	51.7	33	6	BD094291	BD094291 A prepara
C 54	15	51.7	33	6	BD179370	BD179370 A novel p
C 55	15	51.7	41	6	AX514720	AX514720 Sequence
C 56	15	51.7	41	6	AX520728	AX520728 Sequence
C 57	15	51.7	55	8	AJ598912	AJ598912 Arabidops
C 58	14.8	51.0	29	6	AR019319	AR019319 Sequence
C 59	14.8	51.0	29	6	AR061847	AR061847 Sequence
C 60	14.8	51.0	29	6	AR147578	AR147578 Sequence
C 61	14.8	51.0	29	6	BD233978	BD233978 Multiple
C 62	14.8	51.0	29	6	I34733	I34733 Sequence 25
C 63	14.8	51.0	29	6	I67987	I67987 Sequence 25
C 64	14.8	51.0	29	6	AR252838	AR252838 Sequence
C 65	14.8	51.0	32	6	AR061867	AR061867 Sequence

Pred. No. is the number of results predicted by chance to have a

C 66	14.8	51.0	32	6	BD233998	BD233998 Multiple	C 139	13.8	47.6	60	6	AX303607	AX303607 Sequence
C 67	14.8	51.0	32	6	AR252858	AR252858 Sequence	140	13.8	47.6	61	6	AR437950	AR437950 Sequence
C 68	14.8	51.0	80	6	AS2215	Sequence 5	141	13.8	47.6	61	6	AX303592	AX303592 Sequence
C 69	14.6	50.3	25	6	AR206010	Sequence	C 142	13.8	47.6	63	9	HSU91041	U91041 Homo sapien
C 70	14.6	50.3	25	6	AX043294	Sequence	C 143	13.8	47.6	80	8	AJ593415	AJ593415 Arabidops
C 71	14.6	50.3	57	8	AR061021	Sequence	C 144	13.6	46.9	25	6	AX610026	AX610026 Sequence
C 72	14.6	50.3	57	8	AJ591789	Arabidops	C 145	13.6	46.9	30	9	HSCD85719	Z50832 H. sapiens m
C 73	14.6	50.3	73	6	AX909836	Sequence	C 146	13.6	46.9	34	9	AF505532	AF505532 Homo sapi
C 74	14.6	50.3	73	6	BD045369	Sequence	C 147	13.6	46.9	39	9	HUMTCDGA	M28786 Human T-cel
C 75	14.4	49.7	31	6	AX043671	Sequence	148	13.6	46.9	39	9	BD259967	BD259967 Polynucle
C 76	14.4	49.7	31	6	AX425978	Sequence	149	13.6	46.9	41	6	AR179776	AR179776 Sequence
C 77	14.4	49.7	51	6	AX117185	Sequence	150	13.6	46.9	41	6	AX045453	AX045453 Sequence
C 78	14.4	49.7	59	11	AL772710	Arabidops	151	13.6	46.9	41	6	AX045800	AX045800 Sequence
C 79	14.4	49.7	59	11	AL773039	Arabidops	C 152	13.6	46.9	43	8	AJ587991	AJ587991 Arabidops
C 80	14.2	49.0	25	6	AR434675	Sequence	C 153	13.6	46.9	47	6	A84765	A84765 Sequence 10
C 81	14.2	49.0	25	6	AR434676	Sequence	C 154	13.6	46.9	47	6	AR290108	AR290108 Sequence
C 82	14.2	49.0	25	6	AR434677	Sequence	C 155	13.6	46.9	47	6	AR300168	AR300168 Sequence
C 83	14.2	49.0	25	6	AR434678	Sequence	C 156	13.6	46.9	47	6	BD058055	BD058055 Method fo
C 84	14.2	49.0	25	6	AR434679	Sequence	157	13.6	46.9	52	6	BD270556	BD270556 Family of
C 85	14.2	49.0	25	6	AR434680	Sequence	158	13.6	46.9	52	6	AR208953	AR208953 Sequence
C 86	14.2	49.0	25	6	AR434681	Sequence	159	13.6	46.9	52	6	AR228346	AR228346 Sequence
C 87	14.2	49.0	30	6	AX792238	Sequence	160	13.6	46.9	52	6	AX046943	AX046943 Sequence
C 88	14.2	49.0	31	6	AX582577	Sequence	C 161	13.6	46.9	52	6	AX189279	AX189279 Sequence
C 89	14.2	49.0	42	6	BD274270	Identific	162	13.6	46.9	52	6	AX428345	AX428345 Sequence
C 90	14.2	49.0	42	6	BD274278	Identific	163	13.6	46.9	52	6	BD082716	BD082716 Family of
C 91	14.2	49.0	44	6	AX601758	Sequence	164	13.6	46.9	60	6	AX189280	AX189280 Sequence
C 92	14.2	49.0	47	6	AX288361	Sequence	165	13.6	46.9	65	6	AX484957	AX484957 Sequence
C 93	14.2	49.0	65	6	AX483200	Sequence	166	13.6	46.9	69	6	BD161913	BD161913 Recombina
C 94	14.2	49.0	69	6	AR052906	Sequence	C 167	13.6	46.9	72	11	AL806183	AL806183 Arabidops
C 95	14.2	49.0	69	6	AR054269	Sequence	C 168	13.6	46.9	75	11	AL773214	AL773214 Arabidops
C 96	14.2	49.0	69	6	AR054471	Sequence	C 169	13.6	46.9	79	6	AR017735	AR017735 Sequence
C 97	14.2	49.0	69	6	ATH527686	Arabidops	C 170	13.6	46.9	79	6	AR094912	AR094912 Sequence
C 98	14.2	49.0	78	8	ATH527607	Arabidops	C 171	13.6	46.9	79	6	AR165571	AR165571 Sequence
C 99	14.2	49.0	78	8	ATH531507	Arabidops	C 172	13.6	46.9	79	6	AR304769	AR304769 Sequence
C 100	14	48.3	25	6	AX043055	Sequence	C 173	13.6	46.9	80	8	ATH526370	ATH526370 Arabidops
C 101	14	48.3	29	11	AL806194	Arabidops	174	13.6	46.9	80	10	RNSC18	G16776 Rat synapto
C 102	14	48.3	29	11	AL824524	Arabidops	175	13.4	46.2	25	6	AX042556	AX042556 Sequence
C 103	14	48.3	33	11	AL806370	Arabidops	176	13.4	46.2	25	6	AX042557	AX042557 Sequence
C 104	14	48.3	34	11	AL824530	Arabidops	177	13.4	46.2	25	6	AX042570	AX042570 Sequence
C 105	14	48.3	35	11	AL806140	Arabidops	178	13.4	46.2	25	6	AX042575	AX042575 Sequence
C 106	14	48.3	35	11	AL806354	Arabidops	179	13.4	46.2	25	6	AX042625	AX042625 Sequence
C 107	14	48.3	40	11	AL824626	Arabidops	180	13.4	46.2	25	6	AX043147	AX043147 Sequence
C 108	14	48.3	40	11	AL824634	Arabidops	181	13.4	46.2	25	6	AX043173	AX043173 Sequence
C 109	14	48.3	41	6	AR253879	Sequence	182	13.4	46.2	25	6	AX043267	AX043267 Sequence
C 110	14	48.3	41	6	AR410230	Sequence	183	13.4	46.2	25	6	AX043269	AX043269 Sequence
C 111	14	48.3	41	6	AX316543	Sequence	184	13.4	46.2	25	6	AX043288	AX043288 Sequence
C 112	14	48.3	42	11	AL806268	Arabidops	185	13.4	46.2	25	6	AX043479	AX043479 Sequence
C 113	14	48.3	42	11	AL823473	Arabidops	186	13.4	46.2	25	6	AX043558	AX043558 Sequence
C 114	14	48.3	42	11	AL823519	Arabidops	187	13.4	46.2	25	6	AX043602	AX043602 Sequence
C 115	14	48.3	42	11	AL824624	Arabidops	188	13.4	46.2	25	6	AX043611	AX043611 Sequence
C 116	14	48.3	42	11	AL824629	Arabidops	189	13.4	46.2	32	6	AR162666	AR162666 Sequence
C 117	14	48.3	43	11	AL823507	Arabidops	190	13.4	46.2	32	6	AX700013	AX700013 Sequence
C 118	14	48.3	45	11	AL806303	Arabidops	191	13.4	46.2	32	6	BD005937	BD005937 Human B-C
C 119	14	48.3	45	11	AL823500	Arabidops	192	13.4	46.2	32	6	BD185256	BD185256 Sequence
C 120	14	48.3	48	11	EX323648	Arabidops	193	13.4	46.2	34	6	AX282624	AX282624 Sequence
C 121	14	48.3	75	9	AF313283	Homo sapi	194	13.4	46.2	34	6	AX282645	AX282645 Sequence
C 122	13.8	47.6	27	6	AX249915	Sequence	C 195	13.4	46.2	40	6	AR437966	AR437966 Sequence
C 123	13.8	47.6	30	6	AX791584	Sequence	C 196	13.4	46.2	40	6	AX303610	AX303610 Sequence
C 124	13.8	47.6	33	6	BD234015	Multiple	197	13.4	46.2	41	6	AX514585	AX514585 Sequence
C 125	13.8	47.6	33	6	AR252875	Sequence	198	13.4	46.2	41	6	AX520024	AX520024 Sequence
C 126	13.8	47.6	38	9	HSTCSDV21	X59283 H. sapiens m	C 199	13.4	46.2	43	6	AX484576	AX484576 Sequence
C 127	13.8	47.6	38	9	HSTCSDV25	X69287 H. sapiens m	C 200	13.4	46.2	44	6	AX008706	AX008706 Sequence
C 128	13.8	47.6	40	6	E491126	E49126 Novel G pro	C 201	13.4	46.2	45	6	AR008707	AR008707 Sequence
C 129	13.8	47.6	40	6	E50836	E50836 Novel G pro	C 202	13.4	46.2	46	6	AR032430	AR032430 Sequence
C 130	13.8	47.6	41	9	S80780	S80780 gamma delta	C 203	13.4	46.2	46	6	AR032433	AR032433 Sequence
C 131	13.8	47.6	44	6	AX804136	Sequence	C 204	13.4	46.2	46	6	I29170	I29170 Sequence 42
C 132	13.8	47.6	47	6	AR284611	Sequence	C 205	13.4	46.2	46	6	I29173	I29173 Sequence 45
C 133	13.8	47.6	50	6	AR437951	Sequence	C 206	13.4	46.2	46	6	I90844	I90844 Sequence 42
C 134	13.8	47.6	50	6	AX303593	Sequence	C 207	13.4	46.2	46	6	I90847	I90847 Sequence 45
C 135	13.8	47.6	51	6	AX156963	Sequence	C 208	13.4	46.2	46	6	AR209094	AR209094 Sequence
C 136	13.8	47.6	57	6	AR437963	Sequence	C 209	13.4	46.2	46	6	AR209097	AR209097 Sequence
C 137	13.8	47.6	57	6	AX303606	Sequence	C 210	13.4	46.2	47	6	AX378367	AX378367 Sequence
C 138	13.8	47.6	60	6	AR437964	Sequence	C 211	13.4	46.2	50	6	AR032434	AR032434 Sequence

212	13.4	46.2	50	6	I24031	Sequence 13	13	285	44.8	49	6	I17031	I17031 Sequence 42
C 213	13.4	46.2	50	6	I29174	Sequence 46	13	286	44.8	49	6	BD017539	BD017539 Short-cha
C 214	13.4	46.2	50	6	I30848	Sequence 46	13	287	44.8	50	6	AX164867	AX164867 Sequence
C 215	13.4	46.2	51	6	AX209098	Sequence	13	288	44.8	50	6	AX164868	AX164868 Sequence
C 216	13.4	46.2	51	6	AX199419	Sequence	13	289	44.8	50	9	HUMTGVN1	M18908 Human Val-t
C 217	13.4	46.2	51	6	AX199421	Sequence	13	290	44.8	50	9	HUMTGVN1	M18910 Human chime
C 218	13.4	46.2	51	6	AX198444	Sequence	13	291	44.8	51	6	AX160547	AX160547 Sequence
C 219	13.4	46.2	55	8	AJ588102	Arabiidops	13	292	44.8	54	6	I21741	I21741 Sequence 7
C 220	13.4	46.2	61	6	AX899355	Sequence	13	293	44.8	55	1	AF087325	AF087325 Chlamydia
C 221	13.4	46.2	61	6	AX899355	Sequence	13	294	44.8	56	1	AF087325	AF087325 Chlamydia
C 222	13.4	46.2	61	6	BD034888	Sequence	13	295	44.8	59	6	AX905506	AX905506 Sequence
C 223	13.4	46.2	63	8	AF515024	Ginkgo bi	13	296	44.8	59	6	BD041039	BD041039 Sequence
C 224	13.4	46.2	66	8	AJ600346	Arabiidops	13	297	44.8	60	10	AF205765	AF205765 Mus muscu
C 225	13.4	46.2	69	8	HSTRD43A	Human Y43A	13	298	44.8	60	12	SYNANVAA	ME0029 Avian neovi
C 226	13.4	46.2	70	5	CUPCOC22	Y15104 C-japonica	13	299	44.8	63	9	AX152473	AX152473 Homo sapi
C 227	13.4	46.2	72	8	ATH528801	AJ528801 Arabidops	13	300	44.8	64	6	AX798145	AX798145 Sequence
C 228	13.4	46.2	72	8	ATH528801	AJ528801 Arabidops	13	301	44.8	64	6	AX798953	AX798953 Sequence
C 229	13.4	46.2	78	8	ATH531238	AJ531238 Arabidops	13	302	44.8	65	6	AX483133	AX483133 Sequence
C 230	13.4	46.2	25	6	AX434674	Sequence	13	303	44.8	65	6	AX486145	AX486145 Sequence
C 231	13.2	45.5	25	6	AX434674	Sequence	13	304	44.8	66	8	AF515023	AF515023 Ginkgo bi
C 232	13.2	45.5	27	6	I31984	Sequence 23	13	305	44.8	66	10	AX177480	AX177480 Mus muscu
C 233	13.2	45.5	27	6	I31672	Sequence 22	13	306	44.8	68	6	AR242687	AR242687 Sequence
C 234	13.2	45.5	28	6	BD083583	BO083583 A porin g	13	307	44.8	70	6	AR054926	AR054926 Sequence
C 235	13.2	45.5	31	6	AX425725	Sequence	13	308	44.8	70	6	AR066191	AR066191 Sequence
C 236	13.2	45.5	32	6	AX371800	Sequence	13	309	44.8	72	8	ATH528433	AJ528433 Arabidops
C 237	13.2	45.5	37	6	AX465693	Sequence	13	310	44.8	73	6	AX903224	AX903224 Sequence
C 238	13.2	45.5	38	6	AX046687	Sequence	13	311	44.8	73	6	BD038757	BD038757 Sequence
C 239	13.2	45.5	38	6	AX057865	Sequence	13	312	44.8	73	9	S60869	S60869 TCRB (c11/7
C 240	13.2	45.5	38	6	AX115623	Sequence	13	313	44.8	75	6	E02130	E02130 Pseudoknot
C 241	13.2	45.5	38	6	AX634924	Sequence 14	13	314	44.8	76	8	AJ598926	AJ598926 Arabidops
C 242	13.2	45.5	38	6	AX634924	Sequence	13	315	44.8	77	6	AX899700	AX899700 Sequence
C 243	13.2	45.5	40	9	AF505564	Homo sapi	13	316	44.8	77	6	BD035233	BD035233 Sequence
C 244	13.2	45.5	41	6	AX516773	Sequence	13	317	44.8	78	6	AR007410	AR007410 Sequence
C 245	13.2	45.5	47	6	I04390	Sequence 25	13	318	44.8	78	6	BD177994	BD177994 Acylated
C 246	13.2	45.5	47	6	AX290116	Sequence	12.8	319	44.1	16	6	AX255822	AX255822 Sequence
C 247	13.2	45.5	51	6	E22334	DNA encodin	12.8	320	44.1	16	6	AX255865	AX255865 Sequence
C 248	13.2	45.5	51	6	AX204336	Sequence	12.8	321	44.1	18	6	AR293731	AR293731 Sequence
C 249	13.2	45.5	57	9	HSU01098	U91098 Homo sapien	12.8	322	44.1	20	6	AR092414	AR092414 Sequence
C 250	13.2	45.5	59	6	E22349	E22349 DNA encodin	12.8	323	44.1	20	6	AX353716	AX353716 Sequence
C 251	13.2	45.5	59	6	E22349	ME0085 Avian neovi	12.8	324	44.1	20	6	AX082340	AX082340 Sequence
C 252	13.2	45.5	62	9	AB010672	Homo sapi	12.8	325	44.1	20	6	AX613386	AX613386 Sequence
C 253	13.2	45.5	64	6	AX009650	Sequence	12.8	326	44.1	22	6	AX613388	AX613388 Sequence
C 254	13.2	45.5	66	6	HSGDH14A	EL6843 PCR primer	12.8	327	44.1	23	6	BD205443	BD205443 Recombina
C 255	13.2	45.5	66	6	AX356613	Sequence	12.8	328	44.1	24	6	AX173666	AX173666 Sequence
C 256	13.2	45.5	69	6	BD246652	Sequence	12.8	329	44.1	24	6	AX493027	AX493027 Sequence
C 257	13.2	45.5	69	6	AX341695	Sequence	12.8	330	44.1	24	6	BD057100	BD057100 Polymeas
C 258	13.2	45.5	17	6	AX757248	Sequence	12.8	331	44.1	24	10	WMBR242	AX4824 M.musculus
C 259	13	44.8	24	6	AX801575	Sequence	12.8	332	44.1	25	6	AX043436	AX043436 Sequence
C 260	13	44.8	24	6	AX801575	Sequence	12.8	333	44.1	29	6	BD255986	BD255986 Regulatio
C 261	13	44.8	24	6	AX803807	Sequence	12.8	334	44.1	30	6	AS6993	AS6993 Sequence 51
C 262	13	44.8	25	6	AX042898	Sequence	12.8	335	44.1	30	6	AX2012	AX2012 Sequence 15
C 263	13	44.8	25	6	AX042924	Sequence	12.8	336	44.1	31	6	AX223316	AX223316 Sequence
C 264	13	44.8	25	6	AX043101	Sequence	12.8	337	44.1	31	6	AX223401	AX223401 Sequence
C 265	13	44.8	25	6	AX043335	Sequence	12.8	338	44.1	33	6	AR016863	AR016863 Sequence
C 266	13	44.8	27	6	AR039472	Sequence	12.8	339	44.1	33	6	AR020889	AR020889 Sequence
C 267	13	44.8	27	6	AR040432	Sequence	12.8	340	44.1	33	6	AR027212	AR027212 Sequence
C 268	13	44.8	31	6	AX220837	Sequence	12.8	341	44.1	33	6	AR038499	AR038499 Sequence
C 269	13	44.8	31	6	BD002854	Gene comp	12.8	342	44.1	33	6	AR064641	AR064641 Sequence
C 270	13	44.8	34	6	AR089711	Sequence	12.8	343	44.1	33	6	AR067566	AR067566 Sequence
C 271	13	44.8	36	6	AX052576	Sequence	12.8	344	44.1	33	6	I38518	AR083737 Sequence
C 272	13	44.8	38	6	AX08145	Oligonucleo	12.8	345	44.1	33	6	I56993	I38518 Sequence 96
C 273	13	44.8	38	6	AX13246	Oligonucleo	12.8	346	44.1	33	6	I59859	I56993 Sequence 96
C 274	13	44.8	38	6	AX13246	Oligonucleo	12.8	347	44.1	33	6	I75186	I59859 Sequence 96
C 275	13	44.8	38	6	I33196	Sequence 19	12.8	348	44.1	33	6	AR270966	I75186 Sequence 96
C 276	13	44.8	38	6	I40175	Sequence 19	12.8	349	44.1	33	6	AR409734	AR270966 Sequence
C 277	13	44.8	38	6	I40407	Sequence 19	12.8	350	44.1	35	6	AR270966	AR270966 Sequence
C 278	13	44.8	38	6	AX219881	Sequence	12.8	351	44.1	35	11	C75880	C75880 Homo sapien
C 279	13	44.8	40	8	BOL293429	Brassica	12.8	352	44.1	36	6	I39294	I39294 Sequence 33
C 280	13	44.8	41	6	AX515635	Sequence	12.8	353	44.1	36	6	AX635571	AX635571 Sequence
C 281	13	44.8	41	6	AX519230	Sequence	12.8	354	44.1	39	6	AX574443	AX574443 Sequence
C 282	13	44.8	45	10	RATMLV5	M23125 Rat provira	12.8	355	44.1	40	6	AR053634	AR053634 Sequence
C 283	13	44.8	47	6	AX291107	Sequence	12.8	356	44.1	40	6	AX258569	AX258569 Sequence
C 284	13	44.8	48	9	S81456	T cell anti	12.8	357	44.1	40	6	AX496010	AX496010 Sequence

358	12.8	44.1	41	6	AX516373	AX516373 Sequence	431	12.6	43.4	36	6	AR112727	AR112727 Sequence
359	12.8	44.1	41	6	AX518935	AX518935 Sequence	C 432	12.6	43.4	36	6	AR176463	AR176463 Sequence
360	12.8	44.1	41	6	AX518936	AX518936 Sequence	C 433	12.6	43.4	36	6	AR176468	AR176468 Sequence
C 361	12.8	44.1	41	6	AX519782	AX519782 Sequence	C 434	12.6	43.4	36	6	AX468257	AX468257 Sequence
362	12.8	44.1	41	6	AX520403	AX520403 Sequence	C 435	12.6	43.4	41	6	AX516946	AX516946 Sequence
C 363	12.8	44.1	41	6	AR169518	AR169518 Sequence	C 436	12.6	43.4	41	6	AX518206	AX518206 Sequence
C 364	12.8	44.1	43	6	AR169518	AR169518 Sequence	C 437	12.6	43.4	41	6	AX519457	AX519457 Sequence
365	12.8	44.1	45	9	S80711	S80711 gamma delta	C 438	12.6	43.4	42	6	AR139460	AR139460 Sequence
366	12.8	44.1	47	6	AR290646	AR290646 Sequence	C 439	12.6	43.4	42	6	BD274275	BD274275 Identific
367	12.8	44.1	50	6	AX293415	AX293415 Sequence	C 440	12.6	43.4	42	6	BD274283	BD274283 Identific
368	12.8	44.1	50	9	HUMSAU3A07	D49591 Homo sapien	C 441	12.6	43.4	42	6	E22565	E22565 Process for
369	12.8	44.1	50	9	HUMSAU3A10	D49594 Homo sapien	C 442	12.6	43.4	42	6	E22566	E22566 Process for
370	12.8	44.1	54	6	HUMSAU3A66	D49650 Homo sapien	C 443	12.6	43.4	42	6	E25724	E25724 Method for
371	12.8	44.1	54	6	AR098551	AR098551 Sequence	C 444	12.6	43.4	42	6	AR364415	AR364415 Sequence
372	12.8	44.1	54	6	AR108893	AR108893 Sequence	C 445	12.6	43.4	42	10	S77066	S77066 T-cell rece
373	12.8	44.1	54	6	AR268150	AR268150 Sequence	C 446	12.6	43.4	43	6	AR004641	AR004641 Sequence
374	12.8	44.1	54	6	AX009660	AX009660 Sequence	C 447	12.6	43.4	43	6	AR034553	AR034553 Sequence
C 375	12.8	44.1	54	6	AX010922	AX010922 Sequence	C 448	12.6	43.4	43	6	189243	189243 Sequence 4
376	12.8	44.1	57	8	AJ587751	AJ587751 Arabidops	C 449	12.6	43.4	43	8	AJ599099	AJ599099 Arabidops
377	12.8	44.1	57	7	SP17F1D	M14288 Bacterioph	C 450	12.6	43.4	44	6	AX601763	AX601763 Sequence
378	12.8	44.1	60	9	HUMSAU3A41	D49625 Homo sapien	C 451	12.6	43.4	44	6	A76523	A76523 Sequence 4
379	12.8	44.1	60	9	HUMSAU3A42	D49626 Homo sapien	C 452	12.6	43.4	45	6	AR032518	AR032518 Sequence
380	12.8	44.1	60	9	HUMSAU3A44	D49628 Homo sapien	C 453	12.6	43.4	45	6	AR032730	AR032730 Sequence
381	12.8	44.1	61	6	I65507	I65507 Sequence 3	C 454	12.6	43.4	45	6	129358	129358 Sequence 13
C 382	12.8	44.1	63	9	HUMUT68A01	L22543 Human chrom	C 455	12.6	43.4	45	6	129470	129470 Sequence 34
383	12.8	44.1	65	6	AX339385	AX339385 Sequence	C 456	12.6	43.4	45	6	190932	190932 Sequence 13
C 384	12.8	44.1	65	6	AX483725	AX483725 Sequence	C 457	12.6	43.4	45	6	191144	191144 Sequence 34
385	12.8	44.1	65	6	AX483961	AX483961 Sequence	C 458	12.6	43.4	45	6	AR209182	AR209182 Sequence
C 386	12.8	44.1	66	7	PP1C2611I	M13326 Bacterioph	C 459	12.6	43.4	46	6	AR209394	AR209394 Sequence
387	12.8	44.1	66	7	PP1CIN22LI	M13314 Bacterioph	C 460	12.6	43.4	46	6	BD274250	BD274250 Identific
388	12.8	44.1	66	7	PP1CN2611I	M13325 Bacterioph	C 461	12.6	43.4	46	8	AJ522083	AJ522083 Arabidops
C 389	12.8	44.1	69	6	AR171551	AR171551 Sequence	C 462	12.6	43.4	47	6	AX770059	AX770059 Sequence
C 390	12.8	44.1	69	6	AX900803	AX900803 Sequence	C 463	12.6	43.4	48	6	AX003185	AX003185 Sequence
391	12.8	44.1	69	6	AX904939	AX904939 Sequence	C 464	12.6	43.4	48	6	BD195003	BD195003 Equine in
392	12.8	44.1	69	6	BD005571	BD005571 Compositi	C 465	12.6	43.4	49	6	AR403952	AR403952 Sequence
C 393	12.8	44.1	69	6	BD036336	BD036336 Sequence	C 466	12.6	43.4	49	6	AR403953	AR403953 Sequence
394	12.8	44.1	69	6	BD040472	BD040472 Sequence	C 467	12.6	43.4	49	6	AX306319	AX306319 Sequence
395	12.8	44.1	70	8	YSCMTOR12A	M34152 S.cerevisia	C 468	12.6	43.4	49	6	AR032731	AR032731 Sequence
396	12.8	44.1	71	6	AR069299	AR069299 Sequence	C 469	12.6	43.4	50	6	E43956	E43956 Method of n
397	12.8	44.1	71	6	122311	122311 Sequence 39	C 470	12.6	43.4	50	6	129471	129471 Sequence 34
398	12.8	44.1	71	9	S6616781	S66167 sterol regu	C 471	12.6	43.4	50	6	191145	191145 Sequence 34
399	12.8	44.1	72	12	SYNMAC315S	M19736 Cauliflower	C 472	12.6	43.4	50	6	AR209395	AR209395 Sequence
C 400	12.8	44.1	73	8	ATF551623	AJ551623 Arabidops	C 473	12.6	43.4	50	6	AX097512	AX097512 Sequence
C 401	12.8	44.1	76	8	AF276642	AF276642 Silene pa	C 474	12.6	43.4	50	6	AX161234	AX161234 Sequence
402	12.8	44.1	79	6	AX903724	AX903724 Sequence	C 475	12.6	43.4	50	6	AR193638	AR193638 Sequence
C 403	12.8	44.1	79	6	BD039257	BD039257 Sequence	C 476	12.6	43.4	51	6	AR352362	AR352362 Sequence
C 404	12.6	43.4	19	6	I40121	I40121 Sequence 3	C 477	12.6	43.4	51	6	AX199226	AX199226 Sequence
405	12.6	43.4	19	6	AX353501	AX353501 Sequence	C 478	12.6	43.4	52	6	I05057	I05057 Sequence 3
C 406	12.6	43.4	20	6	AX056605	AX056605 Sequence	C 479	12.6	43.4	52	6	AX711215	AX711215 Sequence
C 407	12.6	43.4	21	6	AX097209	AX097209 Sequence	C 480	12.6	43.4	53	6	BD271051	BD271051 Method an
C 408	12.6	43.4	23	6	E49313	E49313 Infectious	C 481	12.6	43.4	54	6	AR258457	AR258457 Sequence
C 409	12.6	43.4	23	6	AR269171	AR269171 Sequence	C 482	12.6	43.4	54	6	AR258457	AR258457 Sequence
C 410	12.6	43.4	23	6	BD015896	BD015896 Infectiou	C 483	12.6	43.4	56	8	NTA38405	NTA38405 Nicotiana
C 411	12.6	43.4	23	6	BD016264	BD016264 Infectiou	C 484	12.6	43.4	59	6	AX917271	AX917271 Sequence
412	12.6	43.4	26	6	AR146828	AR146828 Sequence	C 485	12.6	43.4	59	6	BD052804	BD052804 Sequence
413	12.6	43.4	26	6	E22835	E22835 Promoter se	C 486	12.6	43.4	60	6	A38678	A38678 Sequence 9
414	12.6	43.4	26	8	ATH529956	AJ529956 Arabidops	C 487	12.6	43.4	61	9	AB010652	AB010652 Homo sapi
C 415	12.6	43.4	27	6	AX454931	AX454931 Sequence	C 488	12.6	43.4	62	6	AR086810	AR086810 Sequence
C 416	12.6	43.4	29	6	AX024178	AX024178 Sequence	C 489	12.6	43.4	62	6	AR181439	AR181439 Sequence
417	12.6	43.4	30	6	A27256	A27256 Synthetic G	C 490	12.6	43.4	62	6	AX306321	AX306321 Sequence
418	12.6	43.4	30	6	A56895	A56895 Sequence 8	C 491	12.6	43.4	64	11	HS064685	HS064685 Human chrom
419	12.6	43.4	30	6	AR242736	AR242736 Sequence	C 492	12.6	43.4	65	6	AX306322	AX306322 Sequence
C 420	12.6	43.4	31	6	AX249086	AX249086 Sequence	C 493	12.6	43.4	65	6	AX306323	AX306323 Sequence
C 421	12.6	43.4	31	6	AX274078	AX274078 Sequence	C 494	12.6	43.4	65	6	AX485715	AX485715 Sequence
C 422	12.6	43.4	31	6	AX425595	AX425595 Sequence	C 495	12.6	43.4	66	8	AB028030	AB028030 Candida 8
C 423	12.6	43.4	31	6	AX426095	AX426095 Sequence	C 496	12.6	43.4	69	6	AR055087	AR055087 Sequence
C 424	12.6	43.4	35	6	AR004640	AR004640 Sequence	C 497	12.6	43.4	69	6	AR156336	AR156336 Sequence
C 425	12.6	43.4	35	6	AR034552	AR034552 Sequence	C 498	12.6	43.4	70	6	AX306320	AX306320 Sequence
C 426	12.6	43.4	35	6	189242	189242 Sequence 3	C 499	12.6	43.4	72	6	AR086808	AR086808 Sequence
C 427	12.6	43.4	35	6	AR364414	AR364414 Sequence	C 500	12.6	43.4	74	6	AX701724	AX701724 Sequence
C 428	12.6	43.4	35	11	C75883	C75883 Homo sapien	C 501	12.6	43.4	76	6	AX906465	AX906465 Sequence
429	12.6	43.4	36	6	AR034089	AR034089 Sequence	C 502	12.6	43.4	76	6	BD041998	BD041998 Sequence
430	12.6	43.4	36	6	AR071311	AR071311 Sequence	C 503	12.6	43.4	77	6	AR009153	AR009153 Sequence

C 504	12.6	43.4	77	6	I32419	I32419 Sequence 1	C 577	12.4	42.8	71	9	HUMTCGXF	M12957 Human T-cell
C 505	12.6	43.4	77	8	SOBCPRMF	K00313 S.obliquus	578	12.4	42.8	72	8	ATH528711	AJ528711 Arabidops
C 506	12.6	43.4	78	6	AR129100	AR129100 Sequence	579	12.4	42.8	73	6	AX344130	AX344130 Sequence
C 507	12.6	43.4	78	6	BD243451	BD243451 Nucleic a	580	12.4	42.8	80	11	HUMSWX1361	L41964 Human chrom
C 508	12.6	43.4	79	9	S60076	S60076 T-cell anti	581	12.2	42.1	17	6	AR047002	AR047002 Sequence 17
C 509	12.6	43.4	79	8	AJ593501	AJ593501 Arabidops	582	12.2	42.1	17	6	IS4054	IS4054 Sequence 17
C 510	12.6	43.4	79	8	AX165746	AX165746 Alnus glu	C 583	12.2	42.1	17	6	AR433858	AR433858 Sequence
C 511	12.4	42.8	17	6	AX671567	AX671567 Sequence	C 584	12.2	42.1	17	6	AR433859	AR433859 Sequence
C 512	12.4	42.8	17	6	AX761359	AX761359 Sequence	C 585	12.2	42.1	17	6	AR433860	AR433860 Sequence
C 513	12.4	42.8	22	6	AR403671	AR403671 Sequence	C 586	12.2	42.1	17	6	AX578839	AX578839 Sequence
C 514	12.4	42.8	22	6	AX111296	AX111296 Sequence	C 587	12.2	42.1	20	6	AR315845	AR315845 Sequence
C 515	12.4	42.8	22	6	BD106724	BD106724 Plastid p	C 588	12.2	42.1	20	6	AR337676	AR337676 Sequence
C 516	12.4	42.8	25	6	AX042970	AX042970 Sequence	589	12.2	42.1	20	6	BD131949	BD131949 Oligonuci
C 517	12.4	42.8	25	6	AX609702	AX609702 Sequence	590	12.2	42.1	21	6	AX705969	AX705969 Sequence
C 518	12.4	42.8	25	6	BD061691	BD061691 Antigenic	C 591	12.2	42.1	21	6	BD090087	BD090087 A method
C 519	12.4	42.8	28	6	AR218348	AR218348 Sequence	C 592	12.2	42.1	21	12	AB068906	AB068906 Synthetic
C 520	12.4	42.8	30	6	AR023798	AR023798 Sequence	593	12.2	42.1	22	6	AR374301	AR374301 Sequence
C 521	12.4	42.8	30	6	AR110029	AR110029 Sequence	594	12.2	42.1	24	6	AX493334	AX493334 Sequence
C 522	12.4	42.8	30	6	BD008893	BD008893 High leve	C 595	12.2	42.1	25	6	AR381729	AR381729 Sequence
C 523	12.4	42.8	30	6	BD144237	BD144237 Monoclonal	C 596	12.2	42.1	25	6	AR434673	AR434673 Sequence
C 524	12.4	42.8	31	6	AX221027	AX221027 Sequence	C 597	12.2	42.1	25	6	AR434683	AR434683 Sequence
C 525	12.4	42.8	32	6	E16472	E16472 PCR primer.	C 598	12.2	42.1	25	6	AX006972	AX006972 Sequence
C 526	12.4	42.8	32	6	E27643	E27643 Recombinant	599	12.2	42.1	25	6	AX006973	AX006973 Sequence
C 527	12.4	42.8	33	6	AR219845	AR219845 Sequence	600	12.2	42.1	25	6	AX043040	AX043040 Sequence
C 528	12.4	42.8	34	6	AR381466	AR381466 Sequence	601	12.2	42.1	25	6	AX043439	AX043439 Sequence
C 529	12.4	42.8	34	6	AR381469	AR381469 Sequence	602	12.2	42.1	25	6	AX117932	AX117932 Sequence
C 530	12.4	42.8	37	6	AR003420	AR003420 Sequence	C 603	12.2	42.1	25	6	BD217278	BD217278 Specific
C 531	12.4	42.8	37	6	I21209	I21209 Sequence 55	604	12.2	42.1	25	6	BD217279	BD217279 Specific
C 532	12.4	42.8	37	6	I74476	I74476 Sequence 55	C 605	12.2	42.1	25	6	AX705971	AX705971 Sequence
C 533	12.4	42.8	38	6	AR331044	AR331044 Sequence	C 606	12.2	42.1	29	6	AR018900	AR018900 Sequence
C 534	12.4	42.8	38	6	AX222612	AX222612 Sequence	C 607	12.2	42.1	29	6	AR066528	AR066528 Sequence
C 535	12.4	42.8	40	6	AX138451	AX138451 Sequence	C 608	12.2	42.1	29	6	AR112066	AR112066 Sequence
C 536	12.4	42.8	40	6	BD015619	BD015619 Slidable	C 609	12.2	42.1	29	6	I72245	I72245 Sequence 22
C 537	12.4	42.8	41	6	AX619781	AX619781 Sequence	C 610	12.2	42.1	29	6	I76812	I76812 Sequence 22
C 538	12.4	42.8	42	6	A70930	A70930 Sequence 10	611	12.2	42.1	29	6	AR254606	AR254606 Sequence
C 539	12.4	42.8	42	6	BD003415	BD003415 Soluble p	612	12.2	42.1	30	6	A67214	A67214 Sequence 3
C 540	12.4	42.8	44	6	AR003419	AR003419 Sequence	613	12.2	42.1	30	6	AR076866	AR076866 Sequence
C 541	12.4	42.8	44	6	E55471	E55471 Gene expres	C 614	12.2	42.1	30	6	E55294	E55294 Novel metal
C 542	12.4	42.8	44	6	I21208	I21208 Sequence 54	615	12.2	42.1	30	6	I39990	I39990 Sequence 43
C 543	12.4	42.8	44	6	I74475	I74475 Sequence 54	616	12.2	42.1	30	6	I40002	I40002 Sequence 55
C 544	12.4	42.8	45	6	AX254647	AX254647 Sequence	C 617	12.2	42.1	30	6	AR309877	AR309877 Sequence
C 545	12.4	42.8	45	6	AX774021	AX774021 Sequence	C 618	12.2	42.1	30	6	AR365714	AR365714 Sequence
C 546	12.4	42.8	46	6	AX799825	AX799825 Sequence	C 619	12.2	42.1	30	6	AX793354	AX793354 Sequence
C 547	12.4	42.8	47	6	AR288904	AR288904 Sequence	C 620	12.2	42.1	30	6	BD166020	BD166020 Method of
C 548	12.4	42.8	47	6	AR292024	AR292024 Sequence	C 621	12.2	42.1	31	6	AX223485	AX223485 Sequence
C 549	12.4	42.8	48	6	AR381024	AR381024 Sequence	C 622	12.2	42.1	31	6	AX248729	AX248729 Sequence
C 550	12.4	42.8	48	6	AX079966	AX079966 Sequence	C 623	12.2	42.1	32	6	AR287881	AR287881 Sequence
C 551	12.4	42.8	48	6	BD137448	BD137448 Polymeras	C 624	12.2	42.1	32	6	AX236574	AX236574 Sequence
C 552	12.4	42.8	48	14	SV4MKNV1	K00807 simian viru	625	12.2	42.1	32	6	AX304420	AX304420 Sequence
C 553	12.4	42.8	49	6	AX496194	AX496194 Sequence	C 626	12.2	42.1	32	6	AR151233	AR151233 Sequence
C 554	12.4	42.8	50	6	AX162082	AX162082 Sequence	C 627	12.2	42.1	33	6	BD107554	BD107554 Nucleic a
C 555	12.4	42.8	50	8	AJ587185	AJ587185 Arabidops	628	12.2	42.1	34	6	BD276157	BD276157 Recombina
C 556	12.4	42.8	51	6	AX115997	AX115997 Sequence	629	12.2	42.1	34	6	AR365647	AR365647 Method of
C 557	12.4	42.8	51	6	AX158567	AX158567 Sequence	630	12.2	42.1	34	6	BD166018	BD166018 Method of
C 558	12.4	42.8	51	6	AX161425	AX161425 Sequence	631	12.2	42.1	35	6	A00726	A00726 Oligonucleo
C 559	12.4	42.8	51	6	AX162081	AX162081 Sequence	632	12.2	42.1	35	6	A10025	A10025 Nucleotide
C 560	12.4	42.8	53	6	AX494482	AX494482 Sequence	633	12.2	42.1	36	6	AR068015	AR068015 Sequence
C 561	12.4	42.8	54	6	AX297550	AX297550 Sequence	634	12.2	42.1	36	6	AR120218	AR120218 Sequence
C 562	12.4	42.8	55	14	APH0V1	K01348 Foot and mo	635	12.2	42.1	36	6	I57363	I57363 Sequence 6
C 563	12.4	42.8	56	8	ATH524831	AJ524831 Arabidops	636	12.2	42.1	37	6	AX742083	AX742083 Sequence
C 564	12.4	42.8	60	6	AX766039	AX766039 Sequence	637	12.2	42.1	38	6	AR045510	AR045510 Sequence
C 565	12.4	42.8	60	6	AX776314	AX776314 Sequence	638	12.2	42.1	38	6	AR046016	AR046016 Sequence
C 566	12.4	42.8	62	8	AJ588003	AJ588003 Arabidops	639	12.2	42.1	38	6	AR046084	AR046084 Sequence
C 567	12.4	42.8	63	8	AJ589598	AJ589598 Arabidops	640	12.2	42.1	38	6	AR046535	AR046535 Sequence
C 568	12.4	42.8	65	8	AR179429	AR179429 Sequence	641	12.2	42.1	38	6	I52562	I52562 Sequence 30
C 569	12.4	42.8	65	6	AR205693	AR205693 Sequence	642	12.2	42.1	38	6	I53068	I53068 Sequence 80
C 570	12.4	42.8	65	6	AX073548	AX073548 Sequence	643	12.2	42.1	38	6	I53136	I53136 Sequence 87
C 571	12.4	42.8	65	6	AX482858	AX482858 Sequence	644	12.2	42.1	38	6	I53587	I53587 Sequence 13
C 572	12.4	42.8	65	6	AX486452	AX486452 Sequence	645	12.2	42.1	38	9	S63153	S63153 hprt-hypoxa
C 573	12.4	42.8	66	1	AF178301	AF178301 Chlamydia	646	12.2	42.1	39	6	A07727	A07727 Oligonucleo
C 574	12.4	42.8	66	1	S66739	S66739 omp1-major	C 647	12.2	42.1	39	6	A10026	A10026 Nucleotide
C 575	12.4	42.8	68	6	AR356644	AR356644 Sequence	C 648	12.2	42.1	39	6	E04800	E04800 PCR primer.
C 576	12.4	42.8	71	6	AX573330	AX573330 Sequence	C 649	12.2	42.1	39	6	AR356667	AR356667 Sequence

C 650	12.2	42.1	39	6	BD061900	BD061900 Antigenic	723	12.2	42.1	54	6	BD048253	BD048253 Sequence
651	12.2	42.1	40	6	BD250819	BD250819 Glycosyla	724	12.2	42.1	54	8	ATH523928	ATH523928 Arabidops
652	12.2	42.1	40	6	AR373200	AR373200 Sequence	725	12.2	42.1	55	6	AR102302	AR102302 Sequence
C 653	12.2	42.1	40	6	BD107566	BD107566 Nucleic a	C 726	12.2	42.1	55	6	AX683481	AX683481 Sequence
C 654	12.2	42.1	40	9	HS278086	Z78056 H.sapiens T	C 727	12.2	42.1	57	11	HUMUT5347A	L30843 Human STS U
C 655	12.2	42.1	41	6	AR083451	AR083451 Sequence	728	12.2	42.1	58	6	AR420683	AR420683 Sequence
C 656	12.2	42.1	41	6	AX514045	AX514045 Sequence	729	12.2	42.1	58	6	BD116236	BD116236 EST and e
C 657	12.2	42.1	41	6	AX520514	AX520514 Sequence	C 730	12.2	42.1	59	6	AR171509	AR171509 Sequence
C 658	12.2	42.1	41	6	AX708349	AX708349 Sequence	C 731	12.2	42.1	59	6	I25122	I25122 Sequence 3
C 659	12.2	42.1	41	6	AX708363	AX708363 Sequence	C 732	12.2	42.1	59	6	BD005529	BD005529 Compositi
C 660	12.2	42.1	41	6	AX798427	AX798427 Sequence	733	12.2	42.1	62	6	AX011399	AX011399 Sequence
C 661	12.2	42.1	42	6	AR102301	AR102301 Sequence	734	12.2	42.1	62	6	BD225690	BD225690 Screening
C 662	12.2	42.1	42	6	AX708344	AX708344 Sequence	C 735	12.2	42.1	63	6	I09155	I09155 Sequence 15
C 663	12.2	42.1	42	6	AX708358	AX708358 Sequence	736	12.2	42.1	63	6	AX708346	AX708346 Sequence
C 664	12.2	42.1	42	6	AX798426	AX798426 Sequence	737	12.2	42.1	63	6	AX708360	AX708360 Sequence
C 665	12.2	42.1	43	6	AX483394	AX483394 Sequence	C 738	12.2	42.1	63	9	HSU91085	U91085 Homo sapien
C 666	12.2	42.1	43	6	AX597814	AX597814 Sequence	C 739	12.2	42.1	63	9	HSU91259	U91259 Homo sapien
C 667	12.2	42.1	43	6	AX742082	AX742082 Sequence	740	12.2	42.1	65	6	A06240	A06240 Synthetic H
C 668	12.2	42.1	44	6	AR063773	AR063773 Sequence	741	12.2	42.1	65	6	AX483879	AX483879 Sequence
C 669	12.2	42.1	44	6	I30136	I30136 Sequence 58	742	12.2	42.1	65	6	AX485418	AX485418 Sequence
C 670	12.2	42.1	45	6	AS1851	AS1851 Sequence 15	743	12.2	42.1	65	6	AX486471	AX486471 Sequence
C 671	12.2	42.1	45	6	AR085824	AR085824 Sequence	744	12.2	42.1	65	6	AX486609	AX486609 Sequence
C 672	12.2	42.1	45	6	AR099094	AR099094 Sequence	C 745	12.2	42.1	65	10	AF357452	AF357452 Mus muscu
C 673	12.2	42.1	45	6	AR099108	AR099108 Sequence	C 746	12.2	42.1	66	6	AX288026	AX288026 Sequence
C 674	12.2	42.1	47	6	A07730	A07730 Oligonucleo	C 747	12.2	42.1	67	8	AJ596071	AJ596071 Arabidops
C 675	12.2	42.1	47	6	AR284448	AR284448 Sequence	748	12.2	42.1	67	14	S5785481	S57854 Sigma virus
C 676	12.2	42.1	47	6	AR284640	AR284640 Sequence	749	12.2	42.1	69	6	AX920653	AX920653 Sequence
C 677	12.2	42.1	47	6	AR290551	AR290551 Sequence	750	12.2	42.1	69	6	BD056186	BD056186 Sequence
C 678	12.2	42.1	47	6	AR291223	AR291223 Sequence	751	12.2	42.1	70	6	AR054896	AR054896 Sequence
C 679	12.2	42.1	48	6	A01761	A01761 pT4-m DNA.	752	12.2	42.1	70	6	AR066161	AR066161 Sequence
C 680	12.2	42.1	48	6	A15952	A15952 Oligonucleo	C 753	12.2	42.1	71	10	MMU403504	AJ403504 M.musculu
C 681	12.2	42.1	48	6	BD179481	BD179481 Gene expr	754	12.2	42.1	72	6	AX694993	AX694993 Sequence
C 682	12.2	42.1	48	6	BD188820	BD188820 Gene expr	755	12.2	42.1	72	6	AX708350	AX708350 Sequence
C 683	12.2	42.1	49	6	AX781482	AX781482 Sequence	756	12.2	42.1	72	6	AX708364	AX708364 Sequence
C 684	12.2	42.1	49	6	AX816991	AX816991 Sequence	C 757	12.2	42.1	73	6	AX597817	AX597817 Sequence
C 685	12.2	42.1	49	6	AR164552	AR164552 Sequence	C 758	12.2	42.1	73	6	AX597818	AX597818 Sequence
C 686	12.2	42.1	50	6	AX160546	AX160546 Sequence	C 759	12.2	42.1	74	6	AX096183	AX096183 Sequence
C 687	12.2	42.1	50	6	AX160546	AX160546 Sequence	760	12.2	42.1	75	7	PT5FJ5	PT5FJ5 Bacterioph
C 688	12.2	42.1	50	6	AX160756	AX160756 Sequence	C 761	12.2	42.1	78	6	AR079098	AR079098 Sequence
C 689	12.2	42.1	50	6	AX160958	AX160958 Sequence	C 762	12.2	42.1	78	6	I34799	I34799 Sequence 19
C 690	12.2	42.1	51	1	HIACGC2	Z33385 H.influenza	C 763	12.2	42.1	78	6	I64517	I64517 Sequence 19
C 691	12.2	42.1	51	3	S66469	S66469 12S rRNA (p	764	12.2	42.1	78	6	AR420901	AR420901 Sequence
C 692	12.2	42.1	51	6	A07731	A07731 Oligonucleo	765	12.2	42.1	78	6	BD116454	BD116454 EST and e
C 693	12.2	42.1	51	6	A10029	A10029 Nucleotide	C 766	12.2	42.1	80	6	AS1846	AS1846 Sequence 10
C 694	12.2	42.1	51	6	AR0909025	AR0909025 Sequence	C 767	12.2	42.1	80	6	AS1883	AS1883 Sequence 47
C 695	12.2	42.1	51	6	AR052680	AR052680 Sequence	C 768	12.2	42.1	80	6	AR063776	AR063776 Sequence
C 696	12.2	42.1	51	6	AR050991	AR050991 Sequence	769	12.2	42.1	80	6	AR063777	AR063777 Sequence
C 697	12.2	42.1	51	6	AR057722	AR057722 Sequence	C 770	12.2	42.1	80	6	AR085848	AR085848 Sequence
C 698	12.2	42.1	51	6	AR175113	AR175113 Sequence	C 771	12.2	42.1	80	6	I30139	I30139 Sequence 61
C 699	12.2	42.1	51	6	I74699	I74699 Sequence 39	772	12.2	42.1	80	6	I30140	I30140 Sequence 62
C 700	12.2	42.1	51	6	AR287993	AR287993 Sequence	C 773	12.2	42.1	80	6	AX661812	AX661812 Sequence
C 701	12.2	42.1	51	6	AR360127	AR360127 Sequence	C 774	12.2	42.1	18	6	AX130174	AX130174 Sequence
C 702	12.2	42.1	51	6	AR365606	AR365606 Sequence	775	12.2	42.1	19	6	AR100467	AR100467 Sequence
C 703	12.2	42.1	51	6	AX115517	AX115517 Sequence	776	12.2	42.1	20	6	AR150122	AR150122 Sequence
C 704	12.2	42.1	51	6	AX117933	AX117933 Sequence	777	12.2	42.1	20	6	BD227995	BD227995 Antisense
C 705	12.2	42.1	51	6	AX118337	AX118337 Sequence	778	12.2	42.1	21	6	AR121100	AR121100 Sequence
C 706	12.2	42.1	51	6	AX156964	AX156964 Sequence	779	12.2	42.1	21	6	AR295042	AR295042 Sequence
C 707	12.2	42.1	51	6	AX157249	AX157249 Sequence	780	12.2	42.1	21	6	BD161927	BD161927 Method fo
C 708	12.2	42.1	51	6	AX157567	AX157567 Sequence	781	12.2	42.1	22	6	E26475	E26475 Erysieloth
C 709	12.2	42.1	51	6	AX160385	AX160385 Sequence	782	12.2	42.1	22	6	AR374308	AR374308 Sequence
C 710	12.2	42.1	51	6	AX160464	AX160464 Sequence	783	12.2	42.1	22	6	AR374310	AR374310 Sequence
C 711	12.2	42.1	51	6	AX160545	AX160545 Sequence	784	12.2	42.1	23	6	AX546629	AX546629 Sequence
C 712	12.2	42.1	51	6	AX160967	AX160967 Sequence	785	12.2	42.1	25	6	AX042644	AX042644 Sequence
C 713	12.2	42.1	51	6	AX204359	AX204359 Sequence	786	12.2	42.1	25	6	AX043057	AX043057 Sequence
C 714	12.2	42.1	51	6	MMU86737	U86737 Mus musculu	787	12.2	42.1	25	6	AX043142	AX043142 Sequence
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C 716	12.2	42.1	52	8	AJ599064	AJ599064 Arabidops	789	12.2	42.1	25	6	AX116440	AX116440 Sequence
C 717	12.2	42.1	53	8	ATH527368	AJ527368 Arabidops	C 790	12.2	42.1	25	6	AX610025	AX610025 Sequence
C 718	12.2	42.1	53	8	ATH528555	AJ528555 Arabidops	C 791	12.2	42.1	30	6	AX184137	AX184137 Sequence
C 719	12.2	42.1	54	6	AR286146	AR286146 Sequence	792	12.2	42.1	30	6	AX611219	AX611219 Sequence
C 720	12.2	42.1	54	6	AX009656	AX009656 Sequence	C 793	12.2	42.1	30	9	HUMTCDGCH	M28813 Human T-cell
C 721	12.2	42.1	54	6	AX010918	AX010918 Sequence	C 794	12.2	42.1	31	6	AX220954	AX220954 Sequence
C 722	12.2	42.1	54	6	AX912720	AX912720 Sequence	C 795	12.2	42.1	31	6	AX229093	AX229093 Sequence

C 796	12	41.4	31	6	AX425828	AX425828 Sequence	869	12	41.4	61	6	I05227	I05227 Sequence 9
C 797	12	41.4	31	6	AX426031	AX426031 Sequence	870	12	41.4	61	6	I21907	I21907 Sequence 26
C 798	12	41.4	31	6	AX426069	AX426069 Sequence	871	12	41.4	61	6	I64613	I64613 Sequence 26
C 799	12	41.4	32	6	A87342	A87342 Sequence 67	872	12	41.4	61	6	I87895	I87895 Sequence 26
C 800	12	41.4	32	6	BD057418	BD057418 Protein c	873	12	41.4	61	6	AR238676	AR238676 Sequence
C 801	12	41.4	33	6	AR003120	AR003120 Sequence	874	12	41.4	61	6	AR302676	AR302676 Sequence
C 802	12	41.4	33	6	AR003213	AR003213 Sequence	875	12	41.4	61	6	AX043859	AX043859 Sequence
C 803	12	41.4	33	6	BD20091	BD20091 Sequence 54	876	12	41.4	61	6	AX360855	AX360855 Sequence
C 804	12	41.4	33	6	AX329399	AX329399 Sequence	877	12	41.4	61	6	AX428223	AX428223 Sequence
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C 806	12	41.4	34	6	AX080562	AX080562 Sequence	C 879	12	41.4	61	6	BD049741	BD049741 Sequence
C 807	12	41.4	35	6	I29831	I29831 Sequence 17	880	12	41.4	63	6	AX905178	AX905178 Sequence
C 808	12	41.4	35	9	AF050558	AF050558 Homo sapi	881	12	41.4	63	6	BD040711	BD040711 Sequence
C 809	12	41.4	37	6	AR003121	AR003121 Sequence	882	12	41.4	64	6	I02347	I02347 Sequence 8
C 810	12	41.4	37	6	AR003214	AR003214 Sequence	883	12	41.4	64	6	I07832	I07832 Sequence 8
C 811	12	41.4	37	6	BD273452	BD273452 High sens	884	12	41.4	65	6	AX483243	AX483243 Sequence
C 812	12	41.4	37	6	BD273452	BD273452 Sequence 55	C 885	12	41.4	65	6	AX485707	AX485707 Sequence
C 813	12	41.4	37	6	AX068409	AX068409 Sequence	C 886	12	41.4	65	6	AX486105	AX486105 Sequence
C 814	12	41.4	39	6	A30918	A30918 PCR primer	C 887	12	41.4	65	6	AX486179	AX486179 Sequence
C 815	12	41.4	39	6	AX452098	AX452098 Sequence	C 888	12	41.4	66	6	AR277910	AR277910 Sequence
C 816	12	41.4	40	6	AX456426	AX456426 Sequence	C 889	12	41.4	66	6	AR277911	AR277911 Sequence
C 817	12	41.4	40	12	SYNDISV2	K01416 Ad2/SV40 de	C 890	12	41.4	66	10	AX177462	AX177462 Mus muscu
C 818	12	41.4	40	12	SYNHEYSV2	K01414 Ad2/SV40 de	C 891	12	41.4	67	10	RNU28644	U28644 Rattus norv
C 819	12	41.4	40	12	SYNHYGROB2	M33980 Synthetic h	C 892	12	41.4	69	6	AR410979	AR410979 Sequence
C 820	12	41.4	41	6	AX518043	AX518043 Sequence	C 893	12	41.4	70	6	AX448899	AX448899 Sequence
C 821	12	41.4	41	6	BD274266	BD274266 Identific	C 894	12	41.4	71	1	RSFGCA1	M25019 Plasmid RSP
C 822	12	41.4	44	6	I06248	I06248 Sequence 6	C 895	12	41.4	74	6	AX356676	AX356676 Sequence
C 823	12	41.4	45	6	HUMTCDCGA	M28806 Human T-cell	C 896	12	41.4	74	6	BD175621	BD175621 Expressio
C 824	12	41.4	45	9	AR029113	AR029113 Sequence	C 897	12	41.4	75	6	AX919319	AX919319 Sequence
C 825	12	41.4	47	6	AR035246	AR035246 Sequence	C 898	12	41.4	75	6	BD054852	BD054852 Sequence
C 826	12	41.4	47	6	AR048730	AR048730 Sequence	C 899	12	41.4	76	1	MCTR72	M16765 Mycoplasma
C 827	12	41.4	47	6	AR065925	AR065925 Sequence	C 900	12	41.4	77	9	HUMDP1747	M89847 Human anti
C 828	12	41.4	47	6	AR065925	AR065925 Sequence	C 901	12	41.4	77	14	HSVH5URB	M21439 Herpes viru
C 829	12	41.4	47	6	AR107116	AR107116 Sequence	C 902	12	41.4	78	6	BD265318	BD265318 Compounds
C 830	12	41.4	47	6	AR112707	AR112707 Sequence	C 903	12	41.4	78	6	AR277904	AR277904 Sequence
C 831	12	41.4	47	6	BD248518	BD248518 T cells s	C 904	12	41.4	78	6	AR277905	AR277905 Sequence
C 832	12	41.4	47	6	I73528	I73528 Sequence 3	C 905	12	41.4	78	6	AR401304	AR401304 Sequence
C 833	12	41.4	47	6	AR284651	AR284651 Sequence	C 906	12	41.4	78	6	AX192757	AX192757 Sequence
C 834	12	41.4	47	6	AR291617	AR291617 Sequence	C 907	12	41.4	78	6	AX898364	AX898364 Sequence
C 835	12	41.4	47	6	AX194975	AX194975 Sequence	C 908	12	41.4	78	6	BD033897	BD033897 Sequence
C 836	12	41.4	47	6	AX326771	AX326771 Sequence	C 909	12	41.4	80	6	I34322	I34322 Sequence 21
C 837	12	41.4	50	6	A78842	A78842 Sequence 2	C 910	12	41.4	80	6	AX904773	AX904773 Sequence
C 838	12	41.4	50	6	AX199420	AX199420 Sequence	C 911	12	41.4	80	6	BD040306	BD040306 Sequence
C 839	12	41.4	50	6	AX199422	AX199422 Sequence	C 912	12	41.4	80	8	ATHS20944	AJ520944 Arabidops
C 840	12	41.4	50	6	AX199710	AX199710 Sequence	C 913	11.8	40.7	17	6	BD241209	BD241209 Methods a
C 841	12	41.4	50	6	AX199712	AX199712 Sequence	C 914	11.8	40.7	17	6	AR433861	AR433861 Sequence
C 842	12	41.4	50	10	MUSRR455Y	M27443 Mus musculu	C 915	11.8	40.7	17	6	AR433862	AR433862 Sequence
C 843	12	41.4	51	6	AX114917	AX114917 Sequence	C 916	11.8	40.7	20	6	AR233462	AR233462 Sequence
C 844	12	41.4	51	6	AX115557	AX115557 Sequence	C 917	11.8	40.7	20	6	AX785653	AX785653 Sequence
C 845	12	41.4	51	6	AX116441	AX116441 Sequence	C 918	11.8	40.7	20	6	AX785779	AX785779 Sequence
C 846	12	41.4	51	6	AX161233	AX161233 Sequence	C 919	11.8	40.7	21	6	AX785780	AX785780 Sequence
C 847	12	41.4	51	6	AX161347	AX161347 Sequence	C 920	11.8	40.7	21	6	AX785813	AX785813 Sequence
C 848	12	41.4	51	6	AX161349	AX161349 Sequence	C 921	11.8	40.7	21	9	S63831	S63831 tumor necro
C 849	12	41.4	51	6	AX164997	AX164997 Sequence	C 922	11.8	40.7	22	6	AX203529	AX203529 Sequence
C 850	12	41.4	51	6	AX196651	AX196651 Sequence	C 923	11.8	40.7	24	6	AX445741	AX445741 Sequence
C 851	12	41.4	51	6	AX196653	AX196653 Sequence	C 924	11.8	40.7	25	6	AR434684	AR434684 Sequence
C 852	12	41.4	51	6	AX204335	AX204335 Sequence	C 925	11.8	40.7	25	6	AR434685	AR434685 Sequence
C 853	12	41.4	51	6	AX204505	AX204505 Sequence	C 926	11.8	40.7	25	6	AX042574	AX042574 Sequence
C 854	12	41.4	54	10	QK18	AF090400 Mus muscu	C 927	11.8	40.7	25	6	AX042765	AX042765 Sequence
C 855	12	41.4	54	10	AF224089	AF224089 Mus muscu	C 928	11.8	40.7	25	6	AX043220	AX043220 Sequence
C 856	12	41.4	55	6	AR355572	AR355572 Sequence	C 929	11.8	40.7	25	6	AX043268	AX043268 Sequence
C 857	12	41.4	55	6	AR358906	AR358906 Sequence	C 930	11.8	40.7	25	6	AX043522	AX043522 Sequence
C 858	12	41.4	56	6	AX913897	AX913897 Sequence	C 931	11.8	40.7	25	6	AX043544	AX043544 Sequence
C 859	12	41.4	56	6	BD049430	BD049430 Sequence	C 932	11.8	40.7	25	6	AX043652	AX043652 Sequence
C 860	12	41.4	56	8	AJ591315	AJ591315 Arabidops	C 933	11.8	40.7	25	6	AX043727	AX043727 Sequence
C 861	12	41.4	56	8	AJ201571	AJ201571 Arabidops	C 934	11.8	40.7	25	6	AX043739	AX043739 Sequence
C 862	12	41.4	57	8	AJ589198	AJ589198 Arabidops	C 935	11.8	40.7	25	6	AX448011	AX448011 Sequence
C 863	12	41.4	57	9	MTHSLAS76	X89840 H.sapiens m	C 936	11.8	40.7	25	6	AX487101	AX487101 Sequence
C 864	12	41.4	58	6	I06247	I06247 Sequence 5	C 937	11.8	40.7	26	6	BD262721	BD262721 Informati
C 865	12	41.4	59	6	AR102107	AR102107 Sequence	C 938	11.8	40.7	26	6	AX038144	AX038144 Sequence
C 866	12	41.4	59	6	AR103153	AR103153 Sequence	C 939	11.8	40.7	27	6	AR364272	AR364272 Sequence
C 867	12	41.4	59	6	AX011462	AX011462 Sequence	C 940	11.8	40.7	27	9	HSZ78031	Z78031 H.sapiens T
C 868	12	41.4	59	6	BD225753	BD225753 Screening	C 941	11.8	40.7	27	9	S66421	S66421 ornithine a


```

SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 46)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL     Patent: JP 2002526030-A 209 20-AUG-2002;
COMMENT     ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/209
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .46
            Location/Qualifiers
FEATURES   source
            1. .46
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            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
   |||||:::|||||
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46

RESULT 7
BD274243 46 bp DNA linear PAT 17-JUL-2003
LOCUS     Identification of molecular interaction sites in RNA for novel drug
DEFINITION
ACCESSION BD274243.1 GI:33084011
VERSION   JP 2002526030-A/210.
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL   Patent: JP 2002526030-A 210 20-AUG-2002;
COMMENT   ISIS PHARMACEUTICALS INC
OS        Artificial Sequence
PN        JP 2002526030-A/210
PD        20-AUG-2002
PF        12-MAY-1999 JP 2000548510
PR        12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .46
            Location/Qualifiers
FEATURES   source
            1. .46
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
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Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
   |||||:::|||||
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46

RESULT 8
BD274258 46 bp RNA linear PAT 17-JUL-2003
LOCUS     Identification of molecular interaction sites in RNA for novel drug
DEFINITION
ACCESSION BD274258.1 GI:33084026
VERSION   JP 2002526030-A/225.
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL   Patent: JP 2002526030-A 225 20-AUG-2002;
COMMENT   ISIS PHARMACEUTICALS INC
OS        Artificial Sequence
PN        JP 2002526030-A/225
PD        20-AUG-2002
PF        12-MAY-1999 JP 2000548510
PR        12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1. .46
            Location/Qualifiers
FEATURES   source
            1. .46
            /organism="synthetic construct"
            /mol_type="genomic RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
   |||||:::|||||
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46

RESULT 9
BD274259 46 bp RNA linear PAT 17-JUL-2003
LOCUS     Identification of molecular interaction sites in RNA for novel drug
DEFINITION
ACCESSION BD274259.1 GI:33084027
VERSION   JP 2002526030-A/226.
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL   Patent: JP 2002526030-A 226 20-AUG-2002;
COMMENT   ISIS PHARMACEUTICALS INC
OS        Artificial Sequence
PN        JP 2002526030-A/226
PD        20-AUG-2002
PF        12-MAY-1999 JP 2000548510
PR        12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI

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ACCESSION BD274270
DEPOSITION DD274270 1 CT 33084038

Query M:

Query M:

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Best Local Similarity 60.7%; Pred. No. 0.95; Mismatches 9; Indels 2; Gaps 0;
Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUGUAGCCCAAGGCU 29
|||||:|||||:|||||:|||||:
Db 5 AAGATTCTTTTGTGAAGCCCTACGGCT 32

RESULT 13
BD274238
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274238
VERSION BD274238.1 GI:33084006
KEYWORDS JP 2002526030-A/205.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 205 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.

FEATURES
source
1..46
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 63.0%; Pred. No. 2.8; Mismatches 8; Indels 2; Gaps 0;
Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUGUAGCCCAAGGCU 28
|||||:|||||:|||||:|||||:
Db 20 AAGATTCTTTTGTGAAGCCCTACGGCT 46

RESULT 14
BD274256
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274256
VERSION BD274256.1 GI:33084024
KEYWORDS JP 2002526030-A/223.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 223 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/223
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
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PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.

FEATURES
source
1..46
Location/Qualifiers
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/mol_type='genomic RNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 63.0%; Pred. No. 2.8; Mismatches 8; Indels 2; Gaps 0;
Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUGUAGCCCAAGGCU 28
|||||:|||||:|||||:|||||:
Db 20 AAGATTCTTTTGTGAAGCCCTACGGCT 46

RESULT 15
BD274275
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274275
VERSION BD274275.1 GI:33084043
KEYWORDS JP 2002526030-A/242.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 242 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/242
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
/organism='Artificial Sequence'.

FEATURES
source
1..42
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 5.5; Mismatches 9; Indels 3; Gaps 0;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUCUUUUUGUAGCCCAAGGCU 29
|||||:|||||:|||||:|||||:
Db 5 ATGATTCTTTTGTGAAGCCCTAGGGCT 32

RESULT 16
BD274283
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274283
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Query Match	76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity	59.3%; Pred. No. 17;
Matches	16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY	2 AGAUCUUUUUGUAGGCCCAAGGCC 28 : : : : : : 20 ATGATTCCTTTTGTAGCCCTAGGGCC 46
DB	
RESULT 18	
BD274249	
LOCUS	46 bp DNA linear PAT 17-JUL-2003
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION	BD274249
VERSION	BD274249.1 GI:33084017
KEYWORDS	JP 2002526030-A/216.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 46)
TITLE	Ecker,D.J., Sampath,R., Griffee,R. and Mcneil,J.
JOURNAL	Identification of molecular interaction sites in RNA for novel drug discovery
COMMENT	Patent: JP 2002526030-A 216 20-AUG-2002; ISIS PHARMACEUTICALS INC OS Artificial Sequence PN JP 2002526030-A/216 PD 20-AUG-2002 PF 12-MAY-1999 JP 2000548510 PR 12-MAY-1998 US 60/085032,12-MAY-1998 US 09/076440 PI DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description Of Artificial Sequence: Novel Sequence FH Key Location/Qualifiers FT source 1. .46 FT Location/Qualifiers /organism='Artificial Sequence'. 1. .46 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'
ORIGIN	
Query Match	76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity	59.3%; Pred. No. 17;
Matches	16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY	2 AGAUCUUUUUGUAGGCCCAAGGCC 28 : : : : : : 20 ATGATTCCTTTTGTAGCCCTAGGGCC 46
DB	
RESULT 19	
BD274252	
LOCUS	46 bp DNA linear PAT 17-JUL-2003
DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.
ACCESSION	BD274252
VERSION	BD274252.1 GI:33084020
KEYWORDS	JP 2002526030-A/219.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 46)
AUTHORS	Ecker,D.J., Sampath,R., Griffee,R. and Mcneil,J.
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery
JOURNAL	Patent: JP 2002526030-A 219 20-AUG-2002; ISIS PHARMACEUTICALS INC OS Artificial Sequence PN JP 2002526030-A/219 PD 20-AUG-2002
COMMENT	

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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAGAGCCCAAGGGC 28
|||||:|||||:|||||:|||||
20 ATGATCTCTTTTGTAAAGCCCTAGGGC 46

RESULT 20
BD274253 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274253.1 GI:33084021
VERSION JP 2002526030-A/220.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 220 20-AUG-2002;
OS Artificial Sequence
PN JP 2002526030-A/220
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAGAGCCCAAGGGC 28
|||||:|||||:|||||:|||||
20 ATGATCTCTTTTGTAAAGCCCTAGGGC 46

RESULT 21
BD274257 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
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ACCESSION BD274257.1 GI:33084025
VERSION JP 2002526030-A/224.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 224 20-AUG-2002;
OS Artificial Sequence
PN JP 2002526030-A/224
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAGAGCCCAAGGGC 28
|||||:|||||:|||||:|||||
20 ATGATCTCTTTTGTAGCCCTAGGGC 46

RESULT 22
BD274265 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274265.1 GI:33084033
VERSION JP 2002526030-A/232.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 232 20-AUG-2002;
OS Artificial Sequence
PN JP 2002526030-A/232
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUUUAGAGCCCAAGGGC 28
|||||:|||||:|||||:|||||
20 ATGATCTCTTTTGTAGCCCTAGGGC 46
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[illegible]

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discovery.
ACCESSION BD274279
VERSION BD274279.1 GI:33084047
KEYWORDS JP 2002526030-A/246.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/246
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105 A61K48/00,C12N15/09,C12N15/00 CC Description
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Location/Qualifiers 1..42
FT source /organism='Artificial Sequence'.
FEATURES
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1..42
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 73.1%; Score 21.2; DB 6; Length 42;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUCUUUGUAGGCCCAAGG 27
|||||:|||||:|||||:|||||
Db 5 AAGATCTTTTGTAGCCCTAGGCG 30
RESULT 27
BD274247 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274247
VERSION BD274247.1 GI:33084015
KEYWORDS JP 2002526030-A/214.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 214 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/214
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105 A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers 1..46
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FEATURES
source
1..46
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
discovery.
ACCESSION BD274279
VERSION BD274279.1 GI:33084047
KEYWORDS JP 2002526030-A/246.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/246
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105 A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers 1..42
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1..42
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
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Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUCUUUGUAGGCCCAAGG 27
|||||:|||||:|||||:|||||
Db 5 AAGATCTTTTGTAGCCCTAGGCG 30
RESULT 27
BD274247 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274247
VERSION BD274247.1 GI:33084015
KEYWORDS JP 2002526030-A/214.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 214 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/214
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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VERSION BD274279.1 GI:33084047
KEYWORDS JP 2002526030-A/246.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/246
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105 A61K48/00,C12N15/09,C12N15/00 CC Description
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274263
VERSION BD274263.1 GI:33084031
KEYWORDS JP 2002526030-A/230.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 230 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
FN JP 2002526030-A/230
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274237
VERSION BD274237.1 GI:33084005
KEYWORDS JP 2002526030-A/204.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
Patent: JP 2002526030-A 204 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
LOCUS OS Artificial Sequence
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PN JP 2002526030-A/204
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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of Artificial Sequence: Novel Sequence CC N is any nucleotide
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Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Db 20 AAGATTCCTTTTGTAGGCC 39

RESULT 30
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274251
VERSION BD274251.1 GI:33084019
KEYWORDS JP 2002526030-A/218.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 218 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/218
PD 20-AUG-2002
PF 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
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DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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Db 20 AAGATTCCTTTTGTAGGCC 39

RESULT 31
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DEFINITION discovery.
ACCESSION BD274255
VERSION BD274255.1 GI:33084023
KEYWORDS JP 2002526030-A/222.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 222 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/222
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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ACCESSION BD274255
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KEYWORDS JP 2002526030-A/222.
SOURCE synthetic construct
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REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 222 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/222
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
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DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
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FT misc feature (40)...(46).
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LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274267
VERSION BD274267.1 GI:33084035
KEYWORDS JP 2002526030-A/234.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL Patent: JP 2002526030-A 234 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/234
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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
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DB	22	GATCCTTCTGTAAGCCCTACGGC 46		
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DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.			
ACCESSION	BD274274	1	GI:33084042	
VERSION	JP 2002526030-A/241			
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 42)			
AUTHORS	Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.			
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery			
JOURNAL	Patent: JP 2002526030-A 241 20-AUG-2002;			
COMMENT	ISIS PHARMACEUTICALS INC			
	OS	Artificial Sequence		
	PN	JP 2002526030-A/241		
	PD	20-AUG-2002		
	PF	12-MAY-1999 JP 2000548510		
	PR	12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI		
	DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC			
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DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.			
ACCESSION	BD274282	1	GI:33084050	
VERSION	JP 2002526030-A/249			
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 42)			
AUTHORS	Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.			
TITLE	Identification of molecular interaction sites in RNA for novel drug discovery			
JOURNAL	Patent: JP 2002526030-A 249 20-AUG-2002;			
COMMENT	ISIS PHARMACEUTICALS INC			
	OS	Artificial Sequence		
	PN	JP 2002526030-A/249		
	PD	20-AUG-2002		

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:05:34 ; Search time 179.667 Seconds
(without alignments)

685.702 Million cell updates/sec

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	28	96.6	46	3	AAA71099 Molecular
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57	15.4	53.1	41	6	AB244134	AB244134 Human NDU
58	15.4	53.1	53	7	ABX54825	ABX54825 Bovine ES
59	15.2	52.4	25	5	AA522104	AA522104 Human COL
60	15.2	52.4	33	2	AAV32805	AAV32805 Forward p
61	15.2	52.4	41	6	AB221055	AB221055 Transduc
62	15.2	52.4	41	6	AB221054	AB221054 Transduc
63	15.2	52.4	73	3	AA299748	AA299748 Sense PCR
64	15	51.7	25	8	AC137324	AC137324 Human m
65	15	51.7	40	4	AAH81504	AAH81504 Novel hum
66	15	51.7	40	4	AAH87604	AAH87604 DNA assoc
67	14.8	51.0	36	3	AAA58446	AAA58446 MetC gene
68	14.8	51.0	43	6	AB226815	AB226815 Candida e
69	14.8	51.0	48	6	AB247051	AB247051 Human ATP
70	14.8	51.0	50	6	AB202031	AB202031 Human leu
71	14.6	50.3	27	3	AA257934	AA257934 Petunia n
72	14.6	50.3	27	3	AA250222	AA250222 Reverse p
73	14.6	50.3	51	4	AAH37844	AAH37844 Human SNP
74	14.6	50.3	65	6	AB228212	AB228212 Candida g
75	14.4	49.7	25	3	AA295720	AA295720 HLA DQA1
76	14.4	49.7	25	3	AA296417	AA296417 HLA DQA1
77	14.4	49.7	41	6	ABS60026	ABS60026 Human DNA
78	14.4	49.7	46	6	ABN72001	ABN72001 Streptoco
79	14.2	49.0	25	6	ABS75578	ABS75578 Human PAP
80	14.2	49.0	25	6	ABS75577	ABS75577 Human PAP
81	14.2	49.0	25	6	ABS75573	ABS75573 Human PAP
82	14.2	49.0	25	6	ABS75572	ABS75572 Human PAP
83	14.2	49.0	25	6	ABS75576	ABS75576 Human PAP
84	14.2	49.0	25	6	ABS75574	ABS75574 Human PAP
85	14.2	49.0	25	6	ABS75575	ABS75575 Human PAP
86	14.2	49.0	35	6	ABR01431	ABR01431 Nicotiana
87	14.2	49.0	42	3	AAA71121	AAA71121 Molecular
88	14.2	49.0	42	3	AAA71128	AAA71128 Molecular
89	14.2	49.0	42	3	AAA71120	AAA71120 Molecular
90	14.2	49.0	42	3	AAA71116	AAA71116 Molecular
91	14.2	49.0	42	3	AAA71115	AAA71115 Molecular
92	14.2	49.0	42	3	AAA71129	AAA71129 Molecular
93	14.2	49.0	45	3	AA58441	AA58441 Human Fac
94	14.2	49.0	50	6	AA520796	AA520796 Clostridi
95	14.2	49.0	50	6	AA520794	AA520794 Clostridi
96	14.2	49.0	50	6	AA520795	AA520795 Clostridi

243	13.2	45.5	27	3	AAC68074	Aac68074	Downstrea	316	13.2	45.5	27	3	AAC81703	Aac81703	GAS repor
244	13.2	45.5	27	3	AAC95514	Aac95514	Downstrea	317	13.2	45.5	27	3	AAC66218	Aac66218	Upstream
245	13.2	45.5	27	3	AAC93472	Aac93472	Downstrea	318	13.2	45.5	27	3	AAC66223	Aac66223	Upstream
246	13.2	45.5	27	3	AAC59500	Aac59500	Downstrea	319	13.2	45.5	27	3	AAC22309	Aac22309	Downstrea
247	13.2	45.5	27	3	AAC66403	Aac66403	GAS repor	320	13.2	45.5	27	3	AAC57525	Aac57525	PCR prime
248	13.2	45.5	27	3	AAC58983	Aac58983	GAS repor	321	13.2	45.5	27	3	AAC57530	Aac57530	PCR prime
249	13.2	45.5	27	3	AAC59731	Aac59731	Downstrea	322	13.2	45.5	27	3	AAC59811	Aac59811	Downstrea
250	13.2	45.5	27	3	AAC98766	Aac98766	Downstrea	323	13.2	45.5	27	3	AAA50011	AAA50011	SV40 earl
251	13.2	45.5	27	3	AAA61253	Aaa61253	Downstrea	324	13.2	45.5	27	3	AAA59229	Aaa59229	PCR prime
252	13.2	45.5	27	3	AAF22034	Aaf22034	Downstrea	325	13.2	45.5	27	3	AAA59208	Aaa59208	Downstrea
253	13.2	45.5	27	3	AAC93303	Aac93303	Downstrea	326	13.2	45.5	27	3	AAA73849	Aaa73849	SV40 earl
254	13.2	45.5	27	3	AAA50319	Aaa50319	SV40 prom	327	13.2	45.5	27	3	AAA74405	Aaa74405	SV40 earl
255	13.2	45.5	27	3	RAA50325	Raa50325	SV40 prom	328	13.2	45.5	27	3	AAC69505	Aac69505	Downstrea
256	13.2	45.5	27	3	AAC59042	Aac59042	GAS repor	329	13.2	45.5	27	3	AAC02080	Aac02080	Downstrea
257	13.2	45.5	27	3	AAC79674	Aac79674	Downstrea	330	13.2	45.5	27	3	AAC73858	Aac73858	Downstrea
258	13.2	45.5	27	3	AAC59385	Aac59385	SV40 prom	331	13.2	45.5	27	3	AAF22366	Aaf22366	Downstrea
259	13.2	45.5	27	3	AAZ33680	Aaz33680	3' end of	332	13.2	45.5	27	3	AAD02232	Aad02232	SV40 prom
260	13.2	45.5	27	3	AAZ33684	Aaz33684	PCR prime	333	13.2	45.5	27	4	AAF91851	Aaf91851	SV40 prom
261	13.2	45.5	27	3	AAA26339	Aaa26339	Downstrea	334	13.2	45.5	27	4	AAF91851	Aaf91851	SV40 prom
262	13.2	45.5	27	3	RAAC69448	Raac69448	Downstrea	335	13.2	45.5	27	4	AAS02388	Aas02388	SV40 prom
263	13.2	45.5	27	3	AAC79733	Aac79733	Downstrea	336	13.2	45.5	27	4	AAS02388	Aas02388	SV40 prom
264	13.2	45.5	27	3	AAC59672	Aac59672	SV40 prom	337	13.2	45.5	27	4	AAF23887	Aaf23887	SV40 prom
265	13.2	45.5	27	3	AAC49756	Aaz49756	3' PCR pri	338	13.2	45.5	27	4	AAD05213	Aad05213	SV40 prom
266	13.2	45.5	27	3	AAZ49762	Aaz49762	Downstrea	339	13.2	45.5	27	4	AAD05114	Aad05114	SV40 prom
267	13.2	45.5	27	3	AAC59270	Aac59270	SV40 prom	340	13.2	45.5	27	4	AAD16728	Aad16728	SV40 prom
268	13.2	45.5	27	3	AAC59959	Aac59959	Downstrea	341	13.2	45.5	27	4	AAI98560	Aai98560	Downstrea
269	13.2	45.5	27	3	RAAC78990	Raac78990	Downstrea	342	13.2	45.5	27	4	AAH46818	Aah46818	GAS-SV40
270	13.2	45.5	27	3	AAC78460	Aac78460	SV40 prom	343	13.2	45.5	27	4	AAS28929	Aas28929	Downstrea
271	13.2	45.5	27	3	AAA80599	Aaa80599	Downstrea	344	13.2	45.5	27	4	AAS30254	Aas30254	PCR prime
272	13.2	45.5	27	3	AAA78374	Aaa78374	Downstrea	345	13.2	45.5	27	4	AAS26240	Aas26240	SV40 earl
273	13.2	45.5	27	3	AAA46742	Aaa46742	Primer fo	346	13.2	45.5	27	4	AAD20611	Aad20611	SV40 prom
274	13.2	45.5	27	3	AAZ98010	Aaz98010	SV40 prom	347	13.2	45.5	27	4	AAF81780	Aaf81780	Downstrea
275	13.2	45.5	27	3	AAC69590	Aac69590	Downstrea	348	13.2	45.5	27	4	AAS01453	Aas01453	SV40 prom
276	13.2	45.5	27	3	RAAC69077	Raac69077	Downstrea	349	13.2	45.5	27	4	AAD05046	Aad05046	SV40 prom
277	13.2	45.5	27	3	AAC68018	Aac68018	Downstrea	350	13.2	45.5	27	4	AAD07802	Aad07802	SV40 prom
278	13.2	45.5	27	3	AAC93357	Aac93357	Downstrea	351	13.2	45.5	27	4	AAI11747	Aai11747	PCR prime
279	13.2	45.5	27	3	AAA95094	Aaa95094	Downstrea	352	13.2	45.5	27	4	AAS27607	Aas27607	Novel sig
280	13.2	45.5	27	3	AAA15755	Aaa15755	SV40 prom	353	13.2	45.5	27	4	AAI11464	Aai11464	PCR prime
281	13.2	45.5	27	3	AAZ58632	Aaz58632	SV40 earl	354	13.2	45.5	27	4	AAS27599	Aas27599	Novel sig
282	13.2	45.5	27	3	AAZ58626	Aaz58626	SV40 earl	355	13.2	45.5	27	4	AAS27602	Aas27602	Novel sig
283	13.2	45.5	27	3	AAZ65243	Aaz65243	Downstrea	356	13.2	45.5	27	4	AAS27603	Aas27603	Novel sig
284	13.2	45.5	27	3	RAAC74216	Raac74216	Downstrea	357	13.2	45.5	27	4	AAS27600	Aas27600	Novel sig
285	13.2	45.5	27	3	AAF14508	Aaf14508	Downstrea	358	13.2	45.5	27	4	AAS27604	Aas27604	Novel sig
286	13.2	45.5	27	3	AAZ59617	Aaz59617	Downstrea	359	13.2	45.5	27	4	AAS27601	Aas27601	Novel sig
287	13.2	45.5	27	3	AAZ50694	Aaz50694	Downstrea	360	13.2	45.5	27	4	AAS27606	Aas27606	Novel sig
288	13.2	45.5	27	3	AAZ59559	Aac59559	Downstrea	361	13.2	45.5	27	4	AAI12416	Aai12416	PCR prime
289	13.2	45.5	27	3	AAZ79792	Aaz79792	Downstrea	362	13.2	45.5	27	4	AAD16520	Aad16520	SV40 prom
290	13.2	45.5	27	3	RAAC00079	Raac00079	3' primer	363	13.2	45.5	27	4	ABK41606	Abk41606	Downstrea
291	13.2	45.5	27	3	RAF18427	Aaf18427	Downstrea	364	13.2	45.5	27	4	ABA03110	Aba03110	Downstrea
292	13.2	45.5	27	3	AAC59442	Aac59442	Downstrea	365	13.2	45.5	27	4	AAD20022	Aad20022	SV40 prom
293	13.2	45.5	27	3	AAC69392	Aac69392	Downstrea	366	13.2	45.5	27	4	AAC91259	Aac91259	SV40 prom
294	13.2	45.5	27	3	AAZ97012	Aaz97012	SV40 prom	367	13.2	45.5	27	4	AAF72734	Aaf72734	Downstrea
295	13.2	45.5	27	3	AAA26274	Aaa26274	Downstrea	368	13.2	45.5	27	4	AAS00502	Aas00502	SV40 prom
296	13.2	45.5	27	3	AAA39045	Aaa39045	Downstrea	369	13.2	45.5	27	4	AAD05293	Aad05293	SV40 prom
297	13.2	45.5	27	3	RAAC99234	Raac99234	Downstrea	370	13.2	45.5	27	4	AAS12926	Aas12926	Human car
298	13.2	45.5	27	3	RAAC74273	Raac74273	Downstrea	371	13.2	45.5	27	4	ABA06875	Abao6875	SV40 prom
299	13.2	45.5	27	3	AAAC80524	Aaac80524	Downstrea	372	13.2	45.5	27	4	AAS40778	Aas40778	Downstrea
300	13.2	45.5	27	3	AAAC81079	Aaac81079	Downstrea	373	13.2	45.5	27	4	AAI12118	Aai12118	Human cyt
301	13.2	45.5	27	3	AAZ37782	Aaz37782	PCR prime	374	13.2	45.5	27	4	AAS11959	Aas11959	Human PCR
302	13.2	45.5	27	3	AAZ37777	Aaz37777	PCR prime	375	13.2	45.5	27	4	AAS11952	Aas11952	SV40 PCR
303	13.2	45.5	27	3	AAZ39900	Aac59900	Downstrea	376	13.2	45.5	27	4	AAD16495	Aad16495	SV40 prom
304	13.2	45.5	27	3	AAAC59101	Aac59101	GAS repor	377	13.2	45.5	27	4	AAD02746	Aad02746	GAS-SV40
305	13.2	45.5	27	3	RAA98976	Raa98976	SV40 earl	378	13.2	45.5	27	4	AAF97877	Aaf97877	SV40 prom
306	13.2	45.5	27	3	RAAC98893	Aac98893	SV40 prom	379	13.2	45.5	27	4	AAD16776	Aad16776	Human nov
307	13.2	45.5	27	3	AAA98985	Aaa98985	SV40 earl	380	13.2	45.5	27	4	AAD16743	Aad16743	SV40 prom
308	13.2	45.5	27	3	AAAC93415	Aaac93415	Downstrea	381	13.2	45.5	27	4	AAS30582	Aas30582	PCR prime
309	13.2	45.5	27	3	AAAC63403	Aaac63403	GAS repor	382	13.2	45.5	27	4	AAH77444	Aah77444	SV40 earl
310	13.2	45.5	27	3	AAAC74330	Aaac74330	Downstrea	383	13.2	45.5	27	4	AAD21655	Aad21655	SV40 prom
311	13.2	45.5	27	3	AAA87659	Aaa87659	Downstrea	384	13.2	45.5	27	4	AAC91287	Aac91287	SV40 prom
312	13.2	45.5	27	3	RAA98994	Aaa98994	SV40 earl	385	13.2	45.5	27	4	AAF72342	Aaf72342	Downstrea
313	13.2	45.5	27	3	AAAC81021	Aac81021	Downstrea	386	13.2	45.5	27	4	AAF62746	Aaf62746	3' primer
314	13.2	45.5	27	3	AAAC55183	Aac55183	Downstrea	387	13.2	45.5	27	4	AAH37198	Aah37198	SV40 prom
315	13.2	45.5	27	3	AAAC95455	Aac95455	Downstrea	388	13.2	45.5	27	4	AAD05572	Aad05572	SV40 prom

389	13.2	45.5	27	4	AAD08481	Aad08481	SV40 prom	462	13.2	45.5	27	5	AAS99023	Downstrea
390	13.2	45.5	27	4	AAS08545	Aas08545	SV40 PCR	463	13.2	45.5	27	5	AAS11940	SV40 PCR
391	13.2	45.5	27	4	AAS33045	Aas33045	PCR prime	464	13.2	45.5	27	5	ABK51268	SV40 prom
392	13.2	45.5	27	4	AAD16575	Aad16575	SV40 prom	465	13.2	45.5	27	5	ABK12723	Human DNA
393	13.2	45.5	27	4	AAS34760	Aas34760	Downstrea	466	13.2	45.5	27	5	ABK10997	Downstrea
394	13.2	45.5	27	4	AAD13297	Aad13297	SV40 prom	467	13.2	45.5	27	5	AAC90331	Downstrea
395	13.2	45.5	27	4	AAD13291	Aad13291	SV40 prom	468	13.2	45.5	27	5	AAC90337	Downstrea
396	13.2	45.5	27	4	AAD22304	Aad22304	Simian vi	469	13.2	45.5	27	5	AAF24144	Downstrea
397	13.2	45.5	27	4	AAB83187	Abab3187	Downstrea	470	13.2	45.5	27	5	AAS40063	PCR prime
398	13.2	45.5	27	4	AAB83187	Abab3187	Downstrea	471	13.2	45.5	27	5	AAD16650	SV40 prom
399	13.2	45.5	27	4	AAD03477	Aad03477	Human sec	472	13.2	45.5	27	5	AAS12127	Human lun
400	13.2	45.5	27	4	AAS02633	Aas02633	Human sec	473	13.2	45.5	27	5	AAH46848	GAS-SV40
401	13.2	45.5	27	4	AH31342	Aah31342	SV40 prom	474	13.2	45.5	27	5	AAS00859	SV40 PCR
402	13.2	45.5	27	4	AH31342	Aah31342	SV40 prom	475	13.2	45.5	27	5	Aaf85178	PCR prime
403	13.2	45.5	27	4	AAD07564	Aad07564	SV40 prom	476	13.2	45.5	27	5	AAD05382	SV40 prom
404	13.2	45.5	27	4	AH32515	Aah32515	SV40 prom	477	13.2	45.5	27	5	AAD07648	SV40 prom
405	13.2	45.5	27	4	AH19163	Aah19163	SV40 prom	478	13.2	45.5	27	5	AAD12078	Human TNF
406	13.2	45.5	27	4	AAI19541	Aai19541	Downstrea	479	13.2	45.5	27	5	AAH46926	GAS-SV40
407	13.2	45.5	27	4	AAH48338	Aah48338	SV40 earl	480	13.2	45.5	27	5	AAH46926	GAS-SV40
408	13.2	45.5	27	4	AAD08397	Aad08397	SV40 prom	481	13.2	45.5	27	5	AAC91277	SV40 prom
409	13.2	45.5	27	4	AAF33088	Aaf33088	Downstrea	482	13.2	45.5	27	5	AAC90699	SV40 prom
410	13.2	45.5	27	4	AAS03875	Aas03875	Human sec	483	13.2	45.5	27	5	AAC90699	SV40 prom
411	13.2	45.5	27	4	AAD07763	Aad07763	SV40 prom	484	13.2	45.5	27	5	AAD07698	SV40 prom
412	13.2	45.5	27	4	AAD05485	Aad05485	SV40 prom	485	13.2	45.5	27	5	AAH46926	GAS-SV40
413	13.2	45.5	27	4	AAD04891	Aad04891	SV40 prom	486	13.2	45.5	27	5	AAH46926	GAS-SV40
414	13.2	45.5	27	4	AAD08184	Aad08184	SV40 prom	487	13.2	45.5	27	5	AAH46926	GAS-SV40
415	13.2	45.5	27	4	AAS28876	Aas28876	Human imm	488	13.2	45.5	27	6	ABK51862	Downstrea
416	13.2	45.5	27	4	AAS12063	Aas12063	Human imm	489	13.2	45.5	27	6	ABK51862	Downstrea
417	13.2	45.5	27	4	AAS28877	Aas28877	Human imm	490	13.2	45.5	27	6	ABK51862	Downstrea
418	13.2	45.5	27	4	AAS11962	Aas11962	SV40 PCR	491	13.2	45.5	27	6	ABK51862	Downstrea
419	13.2	45.5	27	4	AAK54944	Aak54944	Downstrea	492	13.2	45.5	27	6	ABK51862	Downstrea
420	13.2	45.5	27	4	ABK11281	Abk11281	SV40 prom	493	13.2	45.5	27	6	ABK51862	Downstrea
421	13.2	45.5	27	4	AAF32750	Aaf32750	SV40 prom	494	13.2	45.5	27	6	ABK51862	Downstrea
422	13.2	45.5	27	4	AAD08338	Aad08338	SV40 prom	495	13.2	45.5	27	6	ABK51862	Downstrea
423	13.2	45.5	27	4	AAI34662	Aai34662	Downstrea	496	13.2	45.5	27	6	ABK51862	Downstrea
424	13.2	45.5	27	4	AAI3462	Aai3462	Extracell	497	13.2	45.5	27	6	ABK51862	Downstrea
425	13.2	45.5	27	4	AAS31462	Aas31462	Human/SV4	498	13.2	45.5	27	6	ABK51862	Downstrea
426	13.2	45.5	27	4	AAS12215	Aas12215	Extracell	499	13.2	45.5	27	6	ABK51862	Downstrea
427	13.2	45.5	27	4	AAH48329	Aah48329	SV40 earl	500	13.2	45.5	27	6	ABK51862	Downstrea
428	13.2	45.5	27	4	AAF32692	Aaf32692	Downstrea	501	13.2	45.5	27	6	ABK51862	Downstrea
429	13.2	45.5	27	4	AAI198607	Aai198607	Human sec	502	13.2	45.5	27	6	ABK51862	Downstrea
430	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	503	13.2	45.5	27	6	ABK51862	Downstrea
431	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	504	13.2	45.5	27	6	ABK51862	Downstrea
432	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	505	13.2	45.5	27	6	ABK51862	Downstrea
433	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	506	13.2	45.5	27	6	ABK51862	Downstrea
434	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	507	13.2	45.5	27	6	ABK51862	Downstrea
435	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	508	13.2	45.5	27	6	ABK51862	Downstrea
436	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	509	13.2	45.5	27	6	ABK51862	Downstrea
437	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	510	13.2	45.5	27	6	ABK51862	Downstrea
438	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	511	13.2	45.5	27	6	ABK51862	Downstrea
439	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	512	13.2	45.5	27	6	ABK51862	Downstrea
440	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	513	13.2	45.5	27	6	ABK51862	Downstrea
441	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	514	13.2	45.5	27	6	ABK51862	Downstrea
442	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	515	13.2	45.5	27	6	ABK51862	Downstrea
443	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	516	13.2	45.5	27	6	ABK51862	Downstrea
444	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	517	13.2	45.5	27	6	ABK51862	Downstrea
445	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	518	13.2	45.5	27	6	ABK51862	Downstrea
446	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	519	13.2	45.5	27	6	ABK51862	Downstrea
447	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	520	13.2	45.5	27	6	ABK51862	Downstrea
448	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	521	13.2	45.5	27	6	ABK51862	Downstrea
449	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	522	13.2	45.5	27	6	ABK51862	Downstrea
450	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	523	13.2	45.5	27	6	ABK51862	Downstrea
451	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	524	13.2	45.5	27	6	ABK51862	Downstrea
452	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	525	13.2	45.5	27	6	ABK51862	Downstrea
453	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	526	13.2	45.5	27	6	ABK51862	Downstrea
454	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	527	13.2	45.5	27	6	ABK51862	Downstrea
455	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	528	13.2	45.5	27	6	ABK51862	Downstrea
456	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	529	13.2	45.5	27	6	ABK51862	Downstrea
457	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	530	13.2	45.5	27	6	ABK51862	Downstrea
458	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	531	13.2	45.5	27	6	ABK51862	Downstrea
459	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	532	13.2	45.5	27	6	ABK51862	Downstrea
460	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	533	13.2	45.5	27	6	ABK51862	Downstrea
461	13.2	45.5	27	4	AAH79222	Aah79222	SV40 earl	534	13.2	45.5	27	6	ABK51862	Downstrea

535	13.2	45.5	27	6	ABV83675	Abv83675 Downstrea	608	13.2	45.5	27	9	ADB94403	AdB94403 Novel hum
536	13.2	45.5	27	6	ABSS54684	Abss54684 SV40 prom	609	13.2	45.5	27	9	ADB94408	AdB94408 Novel hum
537	13.2	45.5	27	6	ABSE6163	Abse6163 5' PCR pr	610	13.2	45.5	27	9	ADB94407	AdB94407 Novel hum
538	13.2	45.5	27	6	AD25362	Ad25362 SV40 prom	611	13.2	45.5	27	9	ADB94410	AdB94410 Novel hum
539	13.2	45.5	27	6	ABL55064	AbL55064 SV40 prom	612	13.2	45.5	27	9	ADB93147	AdB93147 Gamma act
540	13.2	45.5	27	6	ABSG61110	Absg61110 SV40/Gamm	613	13.2	45.5	27	9	ADB94404	AdB94404 Novel hum
541	13.2	45.5	27	6	AD46942	Ad46942 SV40 prom	614	13.2	45.5	27	9	ADB94406	AdB94406 Novel hum
542	13.2	45.5	27	6	ABT16755	Abt16755 GAS-SV40	615	13.2	45.5	27	9	ADB94399	AdB94399 Novel hum
543	13.2	45.5	27	7	ABX16275	Abx16275 SV40 earl	616	13.2	45.5	27	9	AD20055	Adc20055 SV40 prom
544	13.2	45.5	27	7	ABZ81697	Abz81697 SV40 earl	617	13.2	45.5	27	9	ADC06712	Adc06712 Reverse p
545	13.2	45.5	27	7	ABZ81693	Abz81693 SV40 earl	618	13.2	45.5	27	9	ADC25157	Adc25157 Gamma act
546	13.2	45.5	27	7	ACA61941	Ac61941 Gamma act	619	13.2	45.5	27	9	ADC33413	Adc33413 Downstrea
547	13.2	45.5	27	7	ADA55815	Ada55815 Downstrea	620	13.2	45.5	27	9	ADC33413	Adc33413 Downstrea
548	13.2	45.5	27	7	ADA12847	Ada12847 SV40 prom	621	13.2	45.5	27	9	ADC10536	Adc10536 Gamma act
549	13.2	45.5	27	7	ACC78627	Acc78627 GAS repor	622	13.2	45.5	27	9	ADC11074	Adc11074 Extracell
550	13.2	45.5	27	7	ABX95272	Abx95272 Downstrea	623	13.2	45.5	27	9	ADC11073	Adc11073 Extracell
551	13.2	45.5	27	7	ABX95266	Abx95266 Downstrea	624	13.2	45.5	27	9	ADC35294	Adc35294 Gamma act
552	13.2	45.5	27	7	ABZ66884	Abz66884 SV40 prom	625	13.2	45.5	27	9	ADC45918	Adc45918 Gamma act
553	13.2	45.5	27	7	ABZ66884	Abz66884 SV40 prom	626	13.2	45.5	27	9	ADC60419	Adc60419 SV40 prom
554	13.2	45.5	27	7	ABX95971	Abx95971 SV40 prom	627	13.2	45.5	27	9	ADC22094	Adc22094 Human sec
555	13.2	45.5	27	7	ABZ73274	Abz73274 SV40 prom	628	13.2	45.5	27	9	ADC22035	Adc22035 Gamma act
556	13.2	45.5	27	7	ADA39622	Ada39622 Downstrea	629	13.2	45.5	27	9	ADC73371	Adc73371 PCR prime
557	13.2	45.5	27	7	ADA97900	Ada97900 GAS-SV40	630	13.2	45.5	27	9	ADC06492	Adc06492 SV40 prom
558	13.2	45.5	27	7	ABX93495	Abx93495 Gamma act	631	13.2	45.5	27	9	ADC78197	Adc78197 Gamma act
559	13.2	45.5	27	7	ADA47379	Ada47379 SV40 prom	632	13.2	45.5	27	9	ADD19177	Add19177 Gamma act
560	13.2	45.5	27	7	ACD18852	Acc18852 GAS-SV40	633	13.2	45.5	27	9	ADD71421	Add71421 Gamma act
561	13.2	45.5	27	7	ACC50337	Acc50337 Downstrea	634	13.2	45.5	27	9	AD62043	Ad62043 SV40 prom
562	13.2	45.5	27	7	ACA61638	Ac61638 Gamma act	635	13.2	45.5	27	9	AD37522	Ad37522 Human sec
563	13.2	45.5	27	7	ACC62468	Acc62468 SV40 prom	636	13.2	45.5	27	9	AD45198	Ad45198 SV40 prom
564	13.2	45.5	27	7	ABX73962	Abx73962 Human nov	637	13.2	45.5	27	9	ADE11632	Adel1632 SV40 prom
565	13.2	45.5	27	7	ABX73967	Abx73967 Human nov	638	13.2	45.5	27	9	ADE29336	Adel29336 Downstrea
566	13.2	45.5	27	7	ABX73166	Abx73166 Human GAS	639	13.2	45.5	27	9	ADD90189	Add90189 Gamma act
567	13.2	45.5	27	7	ABX73964	Abx73964 Human nov	640	13.2	45.5	27	10	AD86553	Adel86553 Gamma act
568	13.2	45.5	27	7	ABX73965	Abx73965 Human nov	641	13.2	45.5	27	9	AA04581	Aa04581 Polymorph
569	13.2	45.5	27	7	ABX73966	Abx73966 Human nov	642	13.2	45.5	27	9	ABX53174	Abx53174 Bacillus
570	13.2	45.5	27	7	ABX73963	Abx73963 Human nov	643	13.2	45.5	27	9	ABK60175	Abk60175 Human CLC
571	13.2	45.5	27	7	ABX73961	Abx73961 Human nov	644	13.2	45.5	27	9	ABK59935	Abk59935 Human CLC
572	13.2	45.5	27	7	ABX73960	Abx73960 Human nov	645	13.2	45.5	27	9	ACD61432	Adc61432 HCV minus
573	13.2	45.5	27	7	ABZ71183	Abz71183 SV40 prom	646	13.2	45.5	27	9	ABK88425	Abk88425 Vector pC
574	13.2	45.5	27	7	ABZ711562	Abz711562 Gamma act	647	13.2	45.5	27	9	AAH48524	Aah48524 Human TNF
575	13.2	45.5	27	7	ABX57650	Abx57650 GAS conta	648	13.2	45.5	27	9	ABA02362	Ab02362 Human nuc
576	13.2	45.5	27	7	ACD08018	Acc08018 Synthetic	649	13.2	45.5	27	9	ABL54230	AbL54230 Human G-p
577	13.2	45.5	27	7	ADA09453	Ada09453 Human TRI	650	13.2	45.5	27	9	AAI65009	Aai65009 Pax probe
578	13.2	45.5	27	7	ADA09459	Ada09459 Human TRI	651	13.2	45.5	27	9	AAF69812	Aaf69812 Heparin c
579	13.2	45.5	27	7	ADA43816	Ada43816 Downstrea	652	13.2	45.5	27	9	AAF83816	Aaf83816 Dengue-3
580	13.2	45.5	27	7	ADA55955	Ada55955 SV40 prom	653	13.2	45.5	27	9	ABL54532	AbL54532 Pectinatu
581	13.2	45.5	27	7	ADA11384	Ada11384 SV40 prom	654	13.2	45.5	27	9	AAH34817	Aah34817 Human ZSI
582	13.2	45.5	27	8	ABX13245	Abx13245 Nuclear f	655	13.2	45.5	27	9	AAH77723	Aah77723 PCR prime
583	13.2	45.5	27	8	ABX13239	Abx13239 Synthetic	656	13.2	45.5	27	9	AAI32265	Aai32265 Human SNP
584	13.2	45.5	27	8	RAD56344	Rad56344 SV40 prom	657	13.2	45.5	27	9	AAI29197	Aai29197 Human SNP
585	13.2	45.5	27	8	ACD26685	Acc26685 Gamma act	658	13.2	45.5	27	9	AAI33032	Aai33032 Human SNP
586	13.2	45.5	27	8	ACD44924	Acc44924 SV40 prom	659	13.2	45.5	27	9	AAI32240	Aai32240 Human SNP
587	13.2	45.5	27	8	ADA11476	Ada11476 Gamma act	660	13.2	45.5	27	9	AAH39512	Aah39512 Human SNP
588	13.2	45.5	27	8	ACD28269	Acc28269 Gamma act	661	13.2	45.5	27	9	AAH35929	Aah35929 Human spl
589	13.2	45.5	27	8	ACH00352	Acc00352 Gamma act	662	13.2	45.5	27	9	ABN41192	Abn41192 Human spl
590	13.2	45.5	27	8	ACD29552	Acc29552 SV40 prom	663	13.2	45.5	27	9	ABN42261	Abn42261 Human spl
591	13.2	45.5	27	8	ADA27023	Ada27023 SV40 prom	664	13.2	45.5	27	9	ABZ29554	Abz29554 Candida g
592	13.2	45.5	27	8	ADA27244	Ada27244 Human ABC	665	13.2	45.5	27	9	ABN30118	Abn30118 Rat splic
593	13.2	45.5	27	8	ACD82634	Acc82634 Downstrea	666	13.2	45.5	27	9	ABN27823	Abn27823 Rat splic
594	13.2	45.5	27	8	ACD40448	Acc40448 Downstrea	667	13.2	45.5	27	9	ABN57018	Abn57018 Mouse spl
595	13.2	45.5	27	8	ACD26553	Acc26553 SV40 prom	668	13.2	45.5	27	9	ABN57018	Abn57018 Mouse spl
596	13.2	45.5	27	8	ADA07183	Ada07183 SV40 prom	669	13.2	45.5	27	9	AAH97093	Aah97093 Sequence
597	13.2	45.5	27	8	ADB91058	Adb91058 Downstrea	670	13.2	45.5	27	9	AAH97077	Aah97077 Sequence
598	13.2	45.5	27	8	ADB96663	Adb96663 Gamma act	671	13.2	45.5	27	9	AAH18036	Aah18036 C. tracho
599	13.2	45.5	27	8	ADB32067	Adb32067 Gamma act	672	13.2	45.5	27	9	ABK97753	Abk97753 C. tracho
600	13.2	45.5	27	8	ADB59273	Adb59273 GAS promo	673	13.2	45.5	27	9	ABK97769	Abk97769 Da gene p
601	13.2	45.5	27	9	ADB33077	Adb33077 Gamma act	674	13.2	45.5	27	9	AAH51786	Aah51786 C. tracho
602	13.2	45.5	27	9	ADB92797	Adb92797 Gamma act	675	13.2	45.5	27	9	AAV14463	Aav14463 Primer pO
603	13.2	45.5	27	9	ADB47721	Adb47721 Gamma act	676	13.2	45.5	27	9	AAV14463	Aav14463 Primer pO
604	13.2	45.5	27	9	ADB31712	Adb31712 Human nov	677	13.2	45.5	27	9	AAV14463	Aav14463 Primer pO
605	13.2	45.5	27	9	ADB31713	Adb31713 Human nov	678	13.2	45.5	27	9	AAV14463	Aav14463 Primer pO
606	13.2	45.5	27	9	ADB31483	Adb31483 Gamma act	679	13.2	45.5	27	9	AAH96070	Aah96070 16S rRNA
607	13.2	45.5	27	9	ADB94409	Adb94409 Novel hum	680	13.2	45.5	27	9	AAH38767	Aah38767 SNF speci

681	13	44.8	25	6	ABQ12786	Abq12786 Oligonucle	C 754	12.8	44.1	26	2	AAZ25364	Aaz25364 Rat DRM P
682	13	44.8	25	8	ACI30448	ACI30448 Human mic	C 755	12.8	44.1	26	3	AAZ10865	Aaz10865 CycP450 m
683	13	44.8	25	3	ABK50422	ABK50422 Human tra	C 756	12.8	44.1	27	3	AAA08419	Aaa08419 Human tuc
C 684	13	44.8	33	6	ABL54251	ABL54251 Human nuc	C 757	12.8	44.1	30	6	ABX67974	Abx67974 Novel Hel
C 685	13	44.8	38	4	ABK05323	ABK05323 Human NOG	C 758	12.8	44.1	30	6	ABX69591	Abx69591 Novel Hel
C 686	13	44.8	44	9	ADC17368	ADC17368 3' primer	C 759	12.8	44.1	31	2	AAX39384	Aax39384 Human gen
C 687	13	44.8	48	3	AAZ47019	AAZ47019 Primer JC	C 760	12.8	44.1	31	2	AAX39231	Aax39231 Human gen
C 688	13	44.8	48	6	ABN72174	ABN72174 Streptoco	C 761	12.8	44.1	31	4	ABK06479	Abk06479 Human NOG
C 689	13	44.8	49	2	AAV20409	AAV20409 Human eer	C 762	12.8	44.1	31	4	ABK21754	Abk21754 Human ERG
C 690	13	44.8	49	6	ABN52984	ABN52984 Human IGE	C 763	12.8	44.1	31	7	ACA08645	Aca08645 Necroel
C 691	13	44.8	50	4	AAI30837	AAI30837 Human SNP	C 764	12.8	44.1	31	7	ABA05933	Aba05933 Human K-R
C 692	13	44.8	50	4	AAI31756	AAI31756 Human SNP	C 765	12.8	44.1	32	6	ABA05933	Aba05933 Human ubi
C 693	13	44.8	50	6	ABZ07660	ABZ07660 Human leu	C 766	12.8	44.1	39	7	ABX99212	Abx99212 Human CAN
C 694	13	44.8	50	6	ABZ05329	ABZ05329 Human clo	C 767	12.8	44.1	41	6	ABZ48772	Abz48772 Human ald
C 695	13	44.8	51	3	AAZ77092	AAZ77092 Human SNP	C 768	12.8	44.1	41	6	ABZ46261	Abz46261 Human ald
C 696	13	44.8	51	4	AAI29046	AAI29046 Human SNP	C 769	12.8	44.1	42	6	AAQ36455	Aaq36455 Mutagenic
C 697	13	44.8	51	4	AAI28235	AAI28235 Human SNP	C 770	12.8	44.1	42	2	AAQ69592	Aaq69592 Human gen
C 698	13	44.8	51	4	AAI74331	AAI74331 Human sil	C 771	12.8	44.1	45	2	AAQ69380	Aaq69380 Human fib
C 699	13	44.8	51	4	AAH38768	AAH38768 Human SNP	C 772	12.8	44.1	45	2	AAT64054	Aat64054 Human fib
C 700	13	44.8	51	8	ADA94847	ADA94847 Primer JC	C 773	12.8	44.1	45	2	AAT63842	Aat63842 Human fib
C 701	13	44.8	53	2	AAZ47169	AAZ47169 Primer JC	C 774	12.8	44.1	45	2	AAI17130	Aai17130 Test sequ
C 702	13	44.8	54	3	AAZ73969	AAZ73969 GFP Tyr(T	C 775	12.8	44.1	45	2	AAI17342	Aai17342 Test sequ
C 703	13	44.8	54	6	ABQ94682	ABQ94682 Tumour su	C 776	12.8	44.1	45	6	ABK82833	Abk82833 DNA bindi
C 704	13	44.8	55	2	AAQ29522	AAQ29522 Antisense	C 777	12.8	44.1	45	6	ABK82621	Abk82621 DNA bindi
C 705	13	44.8	60	6	ABT12018	ABT12018 E coli ex	C 778	12.8	44.1	45	10	ADH80160	Adh80160 Duplex ol
C 706	13	44.8	60	6	ABN46823	ABN46823 Human spl	C 779	12.8	44.1	45	10	ADH80372	Adh80372 Duplex ol
C 707	13	44.8	60	6	ABN45568	ABN45568 Human spl	C 780	12.8	44.1	47	3	AZ666068	Aaz666068 Human map
C 708	13	44.8	60	6	ABN36148	ABN36148 Human spl	C 781	12.8	44.1	48	9	ADD01530	Add01530 Human del
C 709	13	44.8	60	6	ABN45697	ABN45697 Human spl	C 782	12.8	44.1	50	2	AAQ69593	Aaq69593 Human gen
C 710	13	44.8	65	6	ABZ28160	ABZ28160 Candida g	C 783	12.8	44.1	50	2	AAT64055	Aat64055 Human fib
C 711	13	44.8	65	6	ABZ26554	ABZ26554 Candida e	C 784	12.8	44.1	50	2	AAI17343	Aai17343 Test sequ
C 712	13	44.8	65	6	ABZ26331	ABZ26331 Candida e	C 785	12.8	44.1	50	6	AAI29124	Aai29124 Human SNP
C 713	13	44.8	65	6	ABZ29792	ABZ29792 Candida g	C 786	12.8	44.1	50	6	ABK82834	Abk82834 DNA bindi
C 714	13	44.8	65	6	ABN55646	ABN55646 Mouse spl	C 787	12.8	44.1	50	6	ABZ00746	Abz00746 Human leu
C 715	13	44.8	65	6	ABN29149	ABN29149 Rat spl	C 788	12.8	44.1	50	10	ADH80373	Adh80373 Duplex ol
C 716	13	44.8	65	6	ABN57549	ABN57549 Mouse spl	C 789	12.8	44.1	51	4	AAI27909	Aai27909 Human SNP
C 717	13	44.8	65	6	ABN55388	ABN55388 Mouse spl	C 790	12.8	44.1	54	3	AAZ38935	Aaz38935 hCAT1 bin
C 718	13	44.8	65	6	ABN56758	ABN56758 Mouse spl	C 791	12.8	44.1	54	3	AAZ38741	Aaz38741 hCAT1 bin
C 719	13	44.8	65	6	ABN55469	ABN55469 Mouse spl	C 792	12.8	44.1	57	3	AAA65212	Aaa65212 Savinase
C 720	13	44.8	65	6	ABN57539	ABN57539 Mouse spl	C 793	12.8	44.1	60	6	ABN43416	Abn43416 Human spl
C 721	13	44.8	66	8	AAI62774	AAI62774 Escherich	C 794	12.8	44.1	60	6	ABN33663	Abn33663 Human spl
C 722	13	44.8	67	3	AAZ70174	AAZ70174 TGF-beta-	C 795	12.8	44.1	60	6	ABN44322	Abn44322 Human spl
C 723	13	44.8	70	5	AAZ29228	AAZ29228 Ligand to	C 796	12.8	44.1	60	6	ABN48127	Abn48127 Human spl
C 724	13	44.8	72	2	AAQ67708	AAQ67708 Fragment	C 797	12.8	44.1	60	6	ABN36863	Abn36863 Human spl
C 725	13	44.8	72	2	AAQ67331	AAQ67331 Aait opti	C 798	12.8	44.1	60	6	ABN47014	Abn47014 Human spl
C 726	13	44.8	72	3	AAV18224	AAV18224 Oligomer	C 799	12.8	44.1	60	6	ABN41377	Abn41377 Human spl
C 727	13	44.8	72	3	AAZ16234	AAZ16234 Human sec	C 800	12.8	44.1	60	6	ABN41672	Abn41672 Human spl
C 728	13	44.8	77	4	AAZ01051	AAZ01051 Synthetic	C 801	12.8	44.1	63	2	AAQ26745	Aaq26745 VL-PAL fu
C 729	13	44.8	77	4	AAZ01050	AAZ01050 Synthetic	C 802	12.8	44.1	63	2	AAQ28095	Abz28095 Candida g
C 730	13	44.8	77	6	AAZ22494	AAZ22494 F3R3F1 pr	C 803	12.8	44.1	65	6	ABZ26220	Abz26220 Candida e
C 731	13	44.8	77	6	AAZ22495	AAZ22495 F3R32 pri	C 804	12.8	44.1	65	6	ABZ26704	Abz26704 Candida e
C 732	13	44.8	78	6	ABN53536	ABN53536 Human-mur	C 805	12.8	44.1	65	6	ABZ26664	Abz26664 Candida e
C 733	13	44.8	79	7	ACD94842	ACD94842 Human col	C 806	12.8	44.1	65	6	ABZ27074	Abz27074 Candida e
C 734	12.8	44.1	17	6	ABN74758	ABN74758 Human PAP	C 807	12.8	44.1	65	6	ABZ27244	Abz27244 Candida e
C 735	12.8	44.1	17	6	ABN74756	ABN74756 Human PAP	C 808	12.8	44.1	65	6	ABN28506	Abn28506 Rat spl
C 736	12.8	44.1	18	3	AAZ71110	AAZ71110 Human bla	C 809	12.8	44.1	65	6	ABN52430	Abn52430 Mouse spl
C 737	12.8	44.1	20	7	ABZ46608	ABZ46608 Novel mou	C 810	12.8	44.1	65	6	ABN55121	Abn55121 Mouse spl
C 738	12.8	44.1	20	4	ABZ90675	ABZ90675 Human oli	C 811	12.8	44.1	65	6	ABN55715	Abn55715 Mouse spl
C 739	12.8	44.1	23	2	AAZ33129	AAZ33129 Treponema	C 812	12.8	44.1	68	2	AAV77073	Aav77073 Staphyloc
C 740	12.8	44.1	24	3	AAZ78528	AAZ78528 Mammalian	C 813	12.8	44.1	68	3	AAZ20618	Aaz20618 Human sec
C 741	12.8	44.1	24	3	AAZ29671	AAZ29671 PCR Prime	C 814	12.8	44.1	69	3	AAZ6727	Aaz6727 HIV anti-
C 742	12.8	44.1	25	3	AAZ96631	AAZ96631 Human S4	C 815	12.8	44.1	77	2	AAQ62389	Aaq62389 bioD - bi
C 743	12.8	44.1	25	3	AAZ96387	AAZ96387 HLA DPB1	C 816	12.8	44.1	79	2	AAV64747	Aav64747 HIV anti-
C 744	12.8	44.1	25	6	ABN03205	ABN03205 Human GPM	C 817	12.8	44.1	79	4	AAH24759	Aah24759 Nucleotid
C 745	12.8	44.1	25	6	ABN03204	ABN03204 Human GPM	C 818	12.8	44.1	79	7	ACA74065	Aca74065 Hepatitis
C 746	12.8	44.1	25	6	ABN97741	ABN97741 Human NED	C 819	12.6	43.4	20	7	ABZ90023	Abz90023 Human OLI
C 747	12.8	44.1	25	6	ABN97739	ABN97739 Human NED	C 820	12.6	43.4	21	6	ABK68014	Abk68014 Human FCH
C 748	12.8	44.1	25	6	ABN75581	ABN75581 Human PAP	C 821	12.6	43.4	21	6	ABK70918	Abk70918 Human fam
C 749	12.8	44.1	25	8	ACK25844	ACK25844 Human mic	C 822	12.6	43.4	21	8	ADA15057	Ada15057 Human FCH
C 750	12.8	44.1	25	8	ACI59730	ACI59730 Human mic	C 823	12.6	43.4	21	8	ADB95619	Adb95619 Human FCH
C 751	12.8	44.1	25	8	ACI60358	ACI60358 Human mic	C 824	12.6	43.4	22	7	ACF64048	Acf64048 ESR1 reve
C 752	12.8	44.1	25	8	ACI45682	ACI45682 Human mic	C 825	12.6	43.4	22	6	ABQ01430	Abq01430 Oligonucle
C 753	12.8	44.1	25	8	ACI43897	ACI43897 Human mic	C 826	12.6	43.4	24	6	ABQ06792	Abq06792 Oligonucle

C 827	12.6	43.4	24	6	ABQ66833	Abq66833 Oligonucle	900	12.6	43.4	60	6	ABN50311	Abn50311 Human spl
828	12.6	43.4	24	7	ABZ70877	Abz70877 Human mal	901	12.6	43.4	60	6	ABN41771	Abn41771 Human spl
829	12.6	43.4	25	8	ACI29793	Act29793 Human mic	902	12.6	43.4	60	6	ABN35672	Abn35672 Human spl
C 830	12.6	43.4	25	8	ACH63509	Ach63509 DNA targe	C 903	12.6	43.4	60	6	ABN32296	Abn32296 Human spl
C 831	12.6	43.4	25	8	ACH63383	Ach63383 DNA targe	C 904	12.6	43.4	60	6	ABN42170	Abn42170 Human spl
C 832	12.6	43.4	26	4	AAZ39472	Aaz39472 A. tumefa	C 905	12.6	43.4	60	9	AD887528	Ad887528 Bovine la
C 833	12.6	43.4	26	4	AAF93934	Aaf93934 BAP28 gen	C 906	12.6	43.4	61	7	ABT21735	Abt21735 Breast ca
C 834	12.6	43.4	26	9	ADC84624	Adc84624 p33 cloni	C 907	12.6	43.4	61	7	ABX79947	Abx79947 EST polym
C 835	12.6	43.4	29	2	AAT51441	Aat51441 Mouse hea	C 908	12.6	43.4	64	2	AAT17547	Aat17547 T. littora
C 836	12.6	43.4	29	2	AAQ83497	Aaq83497 MAB 3B9 g	C 909	12.6	43.4	65	6	ABZ26491	Abz26491 Candida e
C 837	12.6	43.4	29	2	AAQ83497	Aaq83497 MAB 3B9 g	C 910	12.6	43.4	65	6	ABZ26491	Abz26491 Candida g
C 838	12.6	43.4	29	2	AAV03498	Aav03498 Mouse gam	C 911	12.6	43.4	65	6	ABZ28341	Abz28341 Candida g
C 839	12.6	43.4	29	2	AAZ38587	Aaz38587 Heavy cha	C 912	12.6	43.4	65	6	ABN30287	Abn30287 Rat splic
C 840	12.6	43.4	29	2	AAZ38495	Aaz38495 PCR prime	C 913	12.6	43.4	65	6	ABN31832	Abn31832 Rat splic
C 841	12.6	43.4	29	2	AAZ79522	Aaz79522 PCR prime	C 914	12.6	43.4	66	6	ABZ53355	Abz53355 Escherich
C 842	12.6	43.4	30	2	AAT51365	Aat51365 Marek's d	C 915	12.6	43.4	72	1	AAZ92382	Aaz92382 Sequence
C 843	12.6	43.4	30	4	AAD21464	Ada21464 O. volvul	C 916	12.6	43.4	74	7	ABZ70378	Abz70378 Streptavi
C 844	12.6	43.4	30	7	ABZ57988	Abz57988 Potato si	C 917	12.6	43.4	75	2	AAQ62654	Aaq62654 Tobacco-m
C 845	12.6	43.4	31	2	AAV67655	Aav67655 Nucleotid	C 918	12.6	43.4	79	4	AAK55455	Aak55455 Human imm
C 846	12.6	43.4	31	7	ACA08357	Aca08357 Necrosis	C 919	12.6	43.4	79	8	AAZ57952	Aaz57952 PCR prime
C 847	12.6	43.4	31	7	ABZ63911	Abz63911 Human H-R	C 920	12.6	43.4	80	2	AAZ42515	Aaz42515 Sequence
C 848	12.6	43.4	31	7	ABZ63853	Abz63853 Human H-R	C 921	12.6	43.4	80	8	AAZ56764	Aaz56764 Target ol
C 849	12.6	43.4	31	7	ABZ62265	Abz62265 Human K-R	C 922	12.6	43.4	80	8	AAZ52315	Aaz52315 Intercala
C 850	12.6	43.4	31	7	ABZ64179	Abz64179 Human H-R	C 923	12.6	43.4	80	8	AAZ57339	Aaz57339 DNA targe
C 851	12.6	43.4	31	7	ACD54727	Acd54727 HBV DNAY	C 924	12.6	43.4	80	9	AD852279	Ad852279 Target DN
C 852	12.6	43.4	31	7	ACD57411	Acd57411 HCV DNAY	C 925	12.6	43.4	15	3	AAZ64356	Aaz64356 Substrate
C 853	12.6	43.4	31	7	ACD61350	Acd61350 HCV DNAY	C 926	12.4	42.8	15	6	ABX01409	Abx01409 Hepatitis
C 854	12.6	43.4	31	7	ACD55579	Acd55579 HCV minus	C 927	12.4	42.8	21	2	AAV38751	Aav38751 PCR prime
C 855	12.6	43.4	32	2	AAV06226	Aav06226 Primer us	C 928	12.4	42.8	22	2	AAV99612	Aav99612 Maize clp
C 856	12.6	43.4	32	3	AAA47264	Aaa47264 Human lig	C 929	12.4	42.8	23	9	ADE14269	Ade14269 Optineuri
C 857	12.6	43.4	33	5	AAI68374	Aai68374 Human lig	C 930	12.4	42.8	24	2	AAQ48650	Aaq48650 Control m
C 858	12.6	43.4	33	6	AAK99345	Aak99345 Human zin	C 931	12.4	42.8	24	2	AAZ16074	Aaz16074 Ikaros ge
C 859	12.6	43.4	33	6	ABZ25189	Abz25189 Peroxidas	C 932	12.4	42.8	24	6	AAZ48844	Aaz48844 Murine Ik
C 860	12.6	43.4	34	2	AAZ78755	Aaz78755 Human RAN	C 933	12.4	42.8	24	7	ABX89729	Abx89729 Interleuk
C 861	12.6	43.4	34	2	AAZ78758	Aaz78758 Human RAN	C 934	12.4	42.8	25	2	AAQ15426	Aaq15426 Vectorsett
C 862	12.6	43.4	35	2	AAZ93671	Aaz93671 Forward p	C 935	12.4	42.8	25	2	AAV02010	Aav02010 Upscream
C 863	12.6	43.4	40	7	ACC59609	Acc59609 S aureus	C 936	12.4	42.8	25	3	AAZ95839	Aaz95839 HLA HLA-A
C 864	12.6	43.4	41	6	ABZ43979	Abz43979 Human glu	C 937	12.4	42.8	25	3	AAZ95839	Aaz95839 HLA HLA-A
C 865	12.6	43.4	41	6	ABZ49571	Abz49571 Human glu	C 938	12.4	42.8	25	3	AAZ95870	Aaz95870 HLA HLA-A
C 866	12.6	43.4	42	3	AAZ71113	Aaz71113 Molecular	C 939	12.4	42.8	25	3	AAZ95870	Aaz95870 HLA HLA-A
C 867	12.6	43.4	42	3	AAZ71118	Aaz71118 Molecular	C 940	12.4	42.8	25	3	AAZ95870	Aaz95870 HLA HLA-A
C 868	12.6	43.4	42	3	AAZ71126	Aaz71126 Molecular	C 941	12.4	42.8	25	3	AAZ95870	Aaz95870 HLA HLA-A
C 869	12.6	43.4	43	3	AAZ75955	Aaz75955 Human PRO	C 942	12.4	42.8	25	6	ABN97742	Abn97742 Human NED
C 870	12.6	43.4	44	3	AAZ71108	Aaz71108 Molecular	C 943	12.4	42.8	25	6	ABN97743	Abn97743 Human NED
C 871	12.6	43.4	45	2	AAT42486	Aat42486 3' primer	C 944	12.4	42.8	25	8	ACI95007	Act95007 Human mic
C 872	12.6	43.4	45	7	ABV93831	Abv93831 Bacillus	C 945	12.4	42.8	25	8	ACI54817	Act54817 Human mic
C 873	12.6	43.4	45	7	ABV93527	Abv93527 Bacillus	C 946	12.4	42.8	25	8	ACI94781	Act94781 Human mic
C 874	12.6	43.4	46	3	AAZ71092	Aaz71092 Molecular	C 947	12.4	42.8	25	8	ACI42213	Act42213 Human mic
C 875	12.6	43.4	47	3	AAZ55952	Aaz55952 Human map	C 948	12.4	42.8	25	8	ACK24015	Ack24015 Human mic
C 876	12.6	43.4	47	3	AAZ56292	Aaz56292 Human map	C 949	12.4	42.8	25	8	ACK24015	Ack24015 Human mic
C 877	12.6	43.4	49	6	ABN71758	Abn71758 Streptoco	C 950	12.4	42.8	26	2	AAQ50450	Aaq50450 Bovine MTP
C 878	12.6	43.4	50	4	AAZ29203	Aaz29203 Human SNP	C 951	12.4	42.8	26	2	AAQ50450	Aaq50450 Bovine MTP
C 879	12.6	43.4	50	4	AAZ29204	Aaz29204 Human SNP	C 952	12.4	42.8	26	3	AAZ62089	Aaz62089 Forward p
C 880	12.6	43.4	50	4	AAZ29345	Aaz29345 Human SNP	C 953	12.4	42.8	26	3	AAZ62089	Aaz62089 Forward p
C 881	12.6	43.4	50	5	ABL00012	AbL00012 Human sll	C 954	12.4	42.8	27	4	AAZ20333	Aaz20333 PCR prime
C 882	12.6	43.4	50	5	ABL00013	AbL00013 Human sll	C 955	12.4	42.8	27	4	AAZ20333	Aaz20333 PCR prime
C 883	12.6	43.4	50	6	ABZ01322	Abz01322 Human leu	C 956	12.4	42.8	29	2	AAZ25844	Aaz25844 Human pol
C 884	12.6	43.4	50	6	ABZ03160	Abz03160 Human leu	C 957	12.4	42.8	29	2	AAZ25844	Aaz25844 Human pol
C 885	12.6	43.4	50	6	ABZ00019	Abz00019 Human leu	C 958	12.4	42.8	29	3	AAA04490	Aaa04490 Polymorph
C 886	12.6	43.4	51	4	AAZ31392	Aaz31392 Human SNP	C 959	12.4	42.8	31	3	AAZ79079	Aaz79079 Human gen
C 887	12.6	43.4	51	4	AAZ31424	Aaz31424 Human SNP	C 960	12.4	42.8	31	4	AAI30740	Aai30740 Human sin
C 888	12.6	43.4	51	4	AAZ29619	Aaz29619 Human SNP	C 961	12.4	42.8	31	7	ABZ63070	Abz63070 Human K-R
C 889	12.6	43.4	51	4	AAZ30782	Aaz30782 Human SNP	C 962	12.4	42.8	31	7	ABZ66157	Abz66157 Human HER
C 890	12.6	43.4	51	4	AAZ31427	Aaz31427 Human SNP	C 963	12.4	42.8	33	2	AAQ74172	Aaq74172 Mouse poo
C 891	12.6	43.4	51	4	AAZ173982	Aaz173982 Human sll	C 964	12.4	42.8	33	4	AAZ05236	Aaz05236 A. fumiga
C 892	12.6	43.4	51	4	AAH90333	Aah90333 Human cto	C 965	12.4	42.8	33	4	AAZ05236	Aaz05236 A. fumiga
C 893	12.6	43.4	51	4	AAH90334	Aah90334 Human cto	C 966	12.4	42.8	33	5	AAH73949	Aah73949 Human alc
C 894	12.6	43.4	53	3	AAH96241	Aah96241 PCR prime	C 967	12.4	42.8	33	6	AAI73030	Aai73030 RNA encod
C 895	12.6	43.4	53	7	ADA48841	Ada48841 PCR prime	C 968	12.4	42.8	33	6	AAI73029	Aai73029 cDNA enco
C 896	12.6	43.4	54	8	ADA36991	Ada36991 Mouse H1	C 969	12.4	42.8	35	4	AAF63484	Aaf63484 Oligonucle
C 897	12.6	43.4	55	5	AAF60029	Aaf60029 Modified	C 970	12.4	42.8	36	2	AAT85337	Aat85337 Spider si
C 898	12.6	43.4	59	9	ADB87653	Adb87653 S. aureus	C 971	12.4	42.8	37	3	AAZ92415	Aaz92415 Plasmid p
C 899	12.6	43.4	60	6	ABN41722	Abn41722 Human spl	C 972	12.4	42.8	38	3	AAZ73295	Aaz73295 Single ba

c 973 12.4 42.8 38 4 ABK08054
 974 12.4 42.8 38 5 AAD11417
 975 12.4 42.8 39 3 AAD40165
 976 12.4 42.8 39 4 AAD09244
 977 12.4 42.8 39 4 AAF88116
 978 12.4 42.8 39 4 AAF88059
 979 12.4 42.8 39 6 ABQ94424
 980 12.4 42.8 39 6 ABQ94423
 981 12.4 42.8 39 6 AAI73042
 982 12.4 42.8 39 6 AAI73041
 983 12.4 42.8 39 7 AB222987
 c 984 12.4 42.8 39 9 ADE25934
 c 985 12.4 42.8 40 6 ABN84179
 986 12.4 42.8 41 6 ABA96651
 987 12.4 42.8 41 6 ABK11368
 988 12.4 42.8 41 6 AB245049
 989 12.4 42.8 41 6 AB247644
 990 12.4 42.8 41 6 ABK89452
 991 12.4 42.8 41 7 AAL56625
 992 12.4 42.8 42 3 AAC69165
 c 993 12.4 42.8 42 7 AAL51937
 c 994 12.4 42.8 43 6 AB227929
 c 995 12.4 42.8 43 6 AB227741
 c 996 12.4 42.8 44 6 AAD29700
 997 12.4 42.8 45 4 AAD09240
 998 12.4 42.8 45 4 AAD10349
 999 12.4 42.8 45 6 AAI73036
 1000 12.4 42.8 45 6 AAI73035

Abk08054 Human CD2
 Aad11417 S. cerevisiae
 Aaa40165 H. pylori
 Aad09244 A. fumigata
 Aaf88116 H. pylori
 Aaf88059 H. pylori
 Abq94424 Tumour su
 Abq94423 Tumour su
 Aai73042 RNA encod
 Aai73041 cDNA enco
 Ab222987 VEE deriv
 Ade25934 GalNac-tr
 Abn84179 Primer HM
 ABA96651 Human tra
 Abk11368 NADH dehy
 Ab245049 Human ATP
 Ab247644 Human ATP
 Abk89452 Human zin
 Aal56625 Probe 2 r
 AAC69165 Human ABC
 Aal51937 Bacillus
 Ab227929 Candida e
 Ab227741 Candida e
 Aad29700 Plasmid p
 Aad09240 A. fumiga
 Aad10349 A. fumiga
 Aai73036 RNA encod
 Aai73035 cDNA enco

ALIGNMENTS

RESULT 1
 AAA70828
 ID AAA70828 standard; RNA; 29 BP.
 AC AAA70828;
 XX
 DT 27-APR-2001 (first entry)
 DE Molecular interaction site RNA #28.
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX Homo sapiens.
 OS WO9958947-A2.
 FN 18-NOV-1999.
 PD 12-MAY-1999; 99WO-US010361.
 PF 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX (ISIS-) ISIS PHARM INC.
 PA Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, McNeil J;
 XX WPI; 2000-086439/07.
 DR Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX Claim 235; Page 235; 405pp; English.
 PS This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds

the target RNA; (b) generating in silico a virtual library of compounds
 predicted or calculated to interact with the molecular interaction site;
 and (c) comparing 3-dimensional (3-D) representations of the target RNA
 with members of the virtual library of compounds to generate a hierarchy
 of the compounds ranked in accordance with their respective ability to
 form physical interactions with the molecular interaction site. The
 method also describes (1) RNA comprising a joined sequence of at least 24
 nucleotides but not more than 70 nucleotides and having secondary
 structure defined by: (a) 3 nucleotides forming a first side of a first
 double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 internal loop region; (c) 4 nucleotides forming a first side of a second
 ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 nucleotides forming a second side of the second ds region; (f) 4
 nucleotides forming a second side of the internal loop region; and (g) 3
 nucleotides forming a second side of the first ds region; (2) a purified
 and isolated RNA fragment comprising the human sequence
 UUUACACAAUUCUAGUUUACAGAAAUUC (II). The methods and products can be
 used for identifying agents which modulate the activity of biomolecules,
 particularly RNA. Such agents can be used as pharmaceutical, agricultural
 or industrial compounds
 SQ Sequence 29 BP; 5 A; 5 C; 7 G; 0 T; 12 U; 0 Other;
 Query Match 100.0%; Score 29; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred No. 0.0026;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 UAUAUUCUUUUUGUUAAGCCUAGGGGCU 29
 |||||
 Db 1 UAUAUUCUUUUUGUUAAGCCUAGGGGCU 29

RESULT 2
 AAA71123
 ID AAA71123 standard; DNA; 42 BP.
 AC AAA71123;
 XX
 DT 27-APR-2001 (first entry)
 DE Molecular interaction site DNA #129.
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX Unidentified.
 OS WO9958947-A2.
 FN 18-NOV-1999.
 PD 12-MAY-1999; 99WO-US010361.
 PF 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX (ISIS-) ISIS PHARM INC.
 PA Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, McNeil J;
 XX WPI; 2000-086439/07.
 DR Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX Example 7; Fig 125; 405pp; English.
 PS This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds

CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; and (g) 3
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUAUCUUAUACAGAAAAC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 42 BP; 9 A; 6 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 3; Length 42;
 Best Local Similarity 58.6%; Pred. No. 0.0027;
 Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUAGUUCUUUUUUAAGCCUAGGGGCU 29
 |||||:|||||:|||||:|||||:
 Db 4 TATGATCTTTTGTAGCCCTAGGGGCT 32

RESULT 3
 AAA71131
 ID AAA71131 standard; RNA; 42 BP.
 XX
 AC AAA71131;
 XX
 DT 27-APR-2001 (first entry)
 DE Molecular interaction site RNA #200.
 DE Modulator; identification; molecular interaction; virtual library; ss.
 XX Unidentified.
 OS
 XX WO9558947-A2.
 XX 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, McNeil J;
 PI WPI; 2000-086439/07.
 DR
 XX
 PT Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 PS Example 7; Fig 126; 405pp; English.
 XX

CC This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA

CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; and (g) 3
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUAUCUUAUACAGAAAAC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 42 BP; 9 A; 6 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 3; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUAGUUCUUUUUUAAGCCUAGGGGCU 29
 |||||:|||||:|||||:|||||:
 Db 4 UAUAGUUCUUUUUUAAGCCUAGGGGCU 32

RESULT 4
 AAA70824
 ID AAA70824 standard; RNA; 45 BP.
 XX
 AC AAA70824;
 XX
 DT 27-APR-2001 (first entry)
 DE Molecular interaction site RNA #24.
 DE Modulator; identification; molecular interaction; virtual library; ss.
 XX Homo sapiens.
 OS
 XX WO9558947-A2.
 XX 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, McNeil J;
 PI WPI; 2000-086439/07.
 DR
 XX
 PT Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 PS Claim 220; Page 232; 405pp; English.
 XX

CC This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA

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cc the target RNA; (b) generating in silico a virtual library of compounds
cc predicted or calculated to interact with the molecular interaction site;
cc and (c) comparing 3-dimensional (3-D) representations of the target RNA
cc with members of the virtual library of compounds to generate a hierarchy

CC of the compounds ranked in accordance with their respective ability to

CC of the compounds ranked in accordance with their respective ability to

CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUUCUAGUUACAGAAAAC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds

XX Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;
 SQ

Query Match 96.6%; Score 28; DB 3; Length 46;
 Best Local Similarity 60.7%; Pred. No. 0.0077;
 Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUAUUCUUUUUUUUAAGCCUAGGGC 28
 :|||:|||||:|||||:|||||
 Db 19 TATGATCTTTTGTAAAGCCCTAGGGC 46

RESULT 7
 AAA71099
 ID AAA71099 standard; DNA; 46 BP.
 XX
 AC AAA71099;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site DNA #122.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.
 OS
 XX WO9958947-A2.
 PN
 XX 18-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-US010361.
 PF
 XX 12-MAY-1998; 98US-00076404.
 PR
 XX 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 XX WPI; 2000-086439/07.
 DR
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The

CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
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 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAAUUCUAGUUACAGAAAAC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds

XX Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 46;
 Best Local Similarity 60.7%; Pred. No. 0.0077;
 Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UUAUUCUUUUUUUUAAGCCUAGGGC 28
 :|||:|||||:|||||:|||||
 Db 19 TATGATCTTTTGTAAAGCCCTAGGGC 46

RESULT 8
 AAA71100
 ID AAA71100 standard; DNA; 46 BP.
 XX
 AC AAA71100;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site DNA #123.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.
 OS
 XX WO9958947-A2.
 PN
 XX 18-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-US010361.
 PF
 XX 12-MAY-1998; 98US-00076404.
 PR
 XX 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 XX WPI; 2000-086439/07.
 DR
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
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CC method also describes (1) RNA comprising a joined sequence of at least 24

CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAUAUUCUAGUUUACAGAAAAUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX
 SQ Sequence 42 BP; 12 A; 7 C; 6 G; 0 T; 17 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 3; Length 42;
 Best Local Similarity 93.1%; Pred. No. 0.074; Mismatches 0; Gaps 0;
 Matches 27; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 UAUAUCUUUUUGUAAGCCUAGGGCU 29
 |||||
 Db 4 UAUAUCUUUUUGUAAGCCUAGGGCU 32

RESULT 11
 AAA71118
 ID AAA71118 standard; DNA; 42 BP.
 XX
 AC AAA71118;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site DNA #124.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX
 OS Unidentified.
 XX
 PN W09958947-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 DR WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX

PS Example 7; Fig 125; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
 CC nucleotides but not more than 70 nucleotides and having secondary
 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an

CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACACAUAUUCUAGUUUACAGAAAAUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds
 XX

SQ Sequence 42 BP; 12 A; 7 C; 6 G; 17 T; 0 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 3; Length 42;
 Best Local Similarity 55.2%; Pred. No. 0.074; Mismatches 11; Gaps 0;
 Matches 16; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAUCUUUUUGUAAGCCUAGGGCU 29
 :|||:|||||:|||||:|||||:
 Db 4 TAAGATTCCTTTTGTAGCCCTACGGCT 32

RESULT 12
 AAA711126
 ID AAA711126 standard; RNA; 42 BP.
 XX
 AC AAA711126;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Molecular interaction site RNA #195.
 XX
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX
 OS Unidentified.
 XX
 PN W09958947-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 12-MAY-1999; 99WO-US010361.
 XX
 PR 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX
 PA (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 XX
 DR WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX

PS Example 7; Fig 126; 405pp; English.

XX This invention describes a novel method for identifying compounds which
 CC modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
 CC with members of the virtual library of compounds to generate a hierarchy
 CC of the compounds ranked in accordance with their respective ability to
 CC form physical interactions with the molecular interaction site. The
 CC method also describes (1) RNA comprising a joined sequence of at least 24
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 CC structure defined by: (a) 3 nucleotides forming a first side of a first
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second

CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
 CC and isolated RNA fragment comprising the human sequence
 CC UUUACAAUAUUCUAGUUUACAGAAAUC (II). The methods and products can be
 CC used for identifying agents which modulate the activity of biomolecules,
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds

XX Sequence 42 BP; 12 A; 7 C; 6 G; 0 T; 17 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 3; Length 42;
 Best Local Similarity 93.1%; Pred. No. 0.074; Mismatches 0; Gaps 0;
 Matches 27; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 1 UUAUAUUUUUUUUAAGCCUAGGGGU 29
 |||||
 Db 4 UUAUAUUUUUUUUAAGCCUAGGGGU 32

RESULT 13

AAA71085
 ID AAA71085 standard; DNA; 46 BP.
 AC AAA71085;
 XX 27-APR-2001 (first entry)
 DT XX
 DE Molecular interaction site DNA #108.
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX Unidentified.
 OS
 XX WO9958947-A2.
 PN 18-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-US010361.
 PF
 XX 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 PI WPI; 2000-086439/07.
 DR
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Example 7; Fig 121; 405pp; English.

PS This invention describes a novel method for identifying compounds which
 XX modulate the activity of a target biomolecule. The method uses 3-
 CC dimensional representations of the biomolecule and a library of compounds
 CC and comprises (a) identifying at least one molecular interaction site of
 CC the target RNA; (b) generating in silico a virtual library of compounds
 CC predicted or calculated to interact with the molecular interaction site;
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 CC internal loop region; (c) 4 nucleotides forming a first side of a second
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 CC

CC nucleotides forming a second side of the second ds region; (f) 4
 CC nucleotides forming a second side of the internal loop region; and (g) 3
 CC nucleotides forming a second side of the first ds region; (2) a purified
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 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
 CC or industrial compounds

XX Sequence 46 BP; 12 A; 7 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 85.5%; Score 24.8; DB 3; Length 46;
 Best Local Similarity 57.1%; Pred. No. 0.21;
 Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UUAUAUUUUUUUUAAGCCUAGGGGC 28
 :|||:|||||:|||||:|||||
 Db 19 TAAGATCTTTTGTAAAGCCCTACGGGC 46

RESULT 14

AAA71103
 ID AAA71103 standard; RNA; 46 BP.
 XX AAA71103;
 AC AAA71103;
 XX 27-APR-2001 (first entry)
 DT XX
 DE Molecular interaction site RNA #179.
 KW Modulator; identification; molecular interaction; virtual library; ss.
 XX Unidentified.
 OS
 XX WO9958947-A2.
 PN 18-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-US010361.
 PF
 XX 12-MAY-1998; 98US-00076404.
 PR 12-MAY-1998; 98US-0085092P.
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
 PI Hofstadler S, Mcneil J;
 PI WPI; 2000-086439/07.
 DR
 XX Identifying compounds which modulate activity of target biomolecules,
 PT used to provide compounds which can be used as pharmacological,
 PT agricultural and industrial compounds.
 XX
 XX Example 7; Fig 122; 405pp; English.

PS This invention describes a novel method for identifying compounds which
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 CC and comprises (a) identifying at least one molecular interaction site of
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 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
 CC internal loop region; (c) 4 nucleotides forming a first side of a second
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
 CC nucleotides forming a second side of the second ds region; (f) 4
 CC

CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
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CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX Sequence 46 BP; 12 A; 7 C; 9 G; 0 T; 18 U; 0 Other;
SQ

Query Match 85.5%; Score 24.8; DB 3; Length 46;
Best Local Similarity 92.9%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGAUCUUUUUUAAGCCUAGGGC 28
Db 19 UAAGAUCUUUUUUAAGCCUAGGGC 46

RESULT 15
AA71114
ID AA71114 standard; RNA; 42 BP.
XX
AC AA71114;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #190.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, McNeil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
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PS Example 7; Fig 122; 405pp; English.
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CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
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CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified

CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAAUAUAGUUUACAGAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX Sequence 42 BP; 11 A; 8 C; 7 G; 0 T; 16 U; 0 Other;
SQ

Query Match 82.1%; Score 23.8; DB 3; Length 42;
Best Local Similarity 92.6%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAUGAUCUUUUUUAAGCCUAGGGC 27
Db 4 UAAGAUCUUUUUUAAGCCUAGGGC 30

RESULT 16
AA71119
ID AA71119 standard; DNA; 42 BP.
XX
AC AA71119;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #125.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, McNeil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 7; Fig 125; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified

CC and isolated RNA fragment comprising the human sequence
CC UUACACAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX
SQ Sequence 42 BP; 11 A; 8 C; 7 G; 16 T; 0 U; 0 Other;
Query Match 82.1%; Score 23.8; DB 3; Length 42;
Best Local Similarity 55.6%; Pred. No. 0.58;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUGUAGCCCUAGGGG 27
|||:||||:||||:||||:||||:|||||
Db 4 TAAGATCTTTTGTGAAGCCCTAGGCG 30

RESULT 17
AAA71127
ID AAA71127 standard; RNA; 42 BP.
XX
AC AAA71127;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #196.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX

PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.

PS Example 7; Fig 126; 405pp; English.

XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence

CC UUACACAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX
SQ Sequence 42 BP; 11 A; 8 C; 7 G; 0 T; 16 U; 0 Other;

Query Match 82.1%; Score 23.8; DB 3; Length 42;
Best Local Similarity 92.6%; Pred. No. 0.58;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUGUAGCCCUAGGGG 27
|||:||||:||||:||||:||||:|||||
Db 4 UAUAUUCUUUUUGUAGCCCUAGGGG 30

RESULT 18
AAA71094
ID AAA71094 standard; DNA; 46 BP.
XX
AC AAA71094;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #117.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
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PT agricultural and industrial compounds.

PS Example 7; Fig 121; 405pp; English.

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CC and isolated RNA fragment comprising the human sequence

UUACACAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be

CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

XX Sequence 46 BP; 12 A; 7 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 82.1%; Score 23.8; DB 3; Length 46;
Best Local Similarity 55.6%; Pred. No. 0.59;
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGUAGCCCUAGGGG 27

19 TAAGATTCTTTTGTAAAGCCCTAGGCG 45

RESULT 19

AAA71110

ID AAA71110 standard; RNA; 46 BP.

AC AAA71110;

DT 27-APR-2001 (first entry)

DE Molecular interaction site RNA #186.

XX Modulator; identification; molecular interaction; virtual library; ss.
XX Unidentified.

XX WO9958947-A2.

XX 18-NOV-1999.

XX 12-MAY-1999; 99WO-US010361.

XX 12-MAY-1998; 98US-00076404.

XX 12-MAY-1998; 98US-0085092P.

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XX Identifying compounds which modulate activity of target biomolecules,

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XX Example 7; Fig 122; 405pp; English.

XX This invention describes a novel method for identifying compounds which
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XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
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XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUUCUAGUUUACAGAAAAC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,

CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

SQ Sequence 46 BP; 12 A; 7 C; 9 G; 0 T; 18 U; 0 Other;

Query Match 82.1%; Score 23.8; DB 3; Length 46;
Best Local Similarity 92.6%; Pred. No. 0.59;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGUAGCCCUAGGGG 27

19 UAAGAUUCUUUUUGUAGCCCUAGGCG 45

RESULT 20

AAA70829

ID AAA70829 standard; RNA; 29 BP.

AC AAA70829;

XX 27-APR-2001 (first entry)

XX Molecular interaction site RNA #29.

XX Modulator; identification; molecular interaction; virtual library; ss.
XX Mus sp.
XX WO9958947-A2.
XX 18-NOV-1999.
XX 12-MAY-1999; 99WO-US010361.
XX 12-MAY-1998; 98US-00076404.
XX 12-MAY-1998; 98US-0085092P.
XX (ISIS-) ISIS PHARM INC.

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XX WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,
XX used to provide compounds which can be used as pharmacological,
XX agricultural and industrial compounds.
XX Claim 235; Page 235; 405pp; English.
XX This invention describes a novel method for identifying compounds which
XX modulate the activity of a target biomolecule. The method uses 3-
XX dimensional representations of the biomolecule and a library of compounds
XX and comprises (a) identifying at least one molecular interaction site of
XX the target RNA; (b) generating in silico a virtual library of compounds
XX predicted or calculated to interact with the molecular interaction site;
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XX nucleotides forming a second side of the second ds region; (f) 4
XX nucleotides forming a second side of the internal loop region; and (g) 3
XX nucleotides forming a second side of the first ds region; (2) a purified
XX and isolated RNA fragment comprising the human sequence
XX UUUACACAAUUCUAGUUUACAGAAAAC (II). The methods and products can be
XX used for identifying agents which modulate the activity of biomolecules,
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural

Query Match 80.0%; Score 23.2; DB 3; Length 42;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGAAGCCUAGGGGCU 29
| | | | | : : : : : | : : : : : | : : : : :
Db 5 AAGATTCCTTTTGTAGCCCAAGGGCT 32

RESULT 25
AAA711116
ID AAA711116 standard; RNA; 42 BP.
XX
AC AAA711116;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #192.
XX
DE Molecular interaction site RNA #192.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
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PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
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XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
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CC and comprises (a) identifying at least one molecular interaction site of
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CC double stranded (ds) region; (c) 4 nucleotides forming a first side of an
CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAAUACUAGUUACAGAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds

SQ Sequence 42 BP; 13 A; 7 C; 7 G; 0 T; 15 U; 0 Other;
Query Match 80.0%; Score 23.2; DB 3; Length 42;

Best Local Similarity 89.3%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGAAGCCUAGGGGCU 29
| | | | | : : : : : | : : : : : | : : : : :
Db 5 AAGAUCUUUUUGAAGCCCAAGGGCU 32

RESULT 26
AAA711115
ID AAA711115 standard; RNA; 42 BP.
XX
AC AAA711115;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #191.
XX
DE Molecular interaction site RNA #191.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
PN WO9558947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
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DR WPI; 2000-086439/07.
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PT used to provide compounds which can be used as pharmacological,
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CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
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CC or industrial compounds

SQ Sequence 42 BP; 13 A; 7 C; 7 G; 0 T; 15 U; 0 Other;
Query Match 80.0%; Score 23.2; DB 3; Length 42;
Best Local Similarity 89.3%; Pred. No. 1.1;

RESULT 34
AAA71107
ID AAA71107 standard; RNA; 46 BP.
XX AC
XX AAA71107;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #183.
XX DE Modulator; identification; molecular interaction; virtual library; ss.
XX KW
XX OS Unidentified.
XX OS
XX PN W0958947-A2.
XX PN
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PF
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PR
XX PA (ISIS-) ISIS PHARM INC.
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XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX PI
XX WI 2000-086439/07.
XX
XX PT Identifying compounds which modulate activity of target biomolecules,
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XX CC
XX CC Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;

```

Query Match          76.8%; Score 22.2; DB 3; Length 46;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AUGAUCUUUUUGUAAGCCCUAGGGGC 28
          ||||| ||||| ||||| |||||
Db       20 AAGAUCUUUUUGUAGCCCCCAGGGC 46

RESULT 35

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```
AAA71088
ID AAA71088 standard; DNA; 46 BP.
XX AC
XX AAA71088;
XX DT
XX 27-APR-2001 (first entry)
XX DE
XX Molecular interaction site DNA #111.
XX KW
XX Modulator; identification; molecular interaction; virtual library; ss.
XX OS
XX Unidentified.
XX PN
XX WO9958947-A2.
XX PD
XX 18-NOV-1999.
XX PF
XX 12-MAY-1999; 99WO-US010361.
XX PR
XX 12-MAY-1998; 98US-00076404.
XX PR
XX 12-MAY-1998; 98US-0085092P.
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XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
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XX SQ
XX Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;
XX
Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUUUUAAGCCUAGGGC 28
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGATTCCTTTTGAAGCCCAAGGGC 46
| | | | | | | | | | | | | | | | | | | |
RESULT 36
AAA71105
ID AAA71090 standard; DNA; 46 BP.
XX AC
XX AAA71105;
XX DT
XX 27-APR-2001 (first entry)
XX DE
XX Molecular interaction site RNA #181.
XX KW
XX Modulator; identification; molecular interaction; virtual library; ss.
XX OS
XX Unidentified.
XX PN
XX WO9958947-A2.
XX PD
XX 18-NOV-1999.
XX PF
XX 12-MAY-1999; 99WO-US010361.
XX PR
XX 12-MAY-1998; 98US-00076404.
XX PR
XX 12-MAY-1998; 98US-0085092P.
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XX WPI; 2000-086439/07.
XX DR
XX WPI; 2000-086439/07.
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XX the target RNA; (b) generating in silico a virtual library of compounds
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XX nucleotides forming a second side of the first ds region; (2) a purified
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XX and isolated RNA fragment comprising the human sequence
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XX particularly RNA. Such agents can be used as pharmaceutical, agricultural
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XX Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;
XX
Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUUUUAAGCCUAGGGC 28
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGAUUUUUUUUUAAGCCCAAGGGC 46
| | | | | | | | | | | | | | | | | | | |
RESULT 37
AAA71090
ID AAA71090 standard; DNA; 46 BP.
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XX AC AAA71090;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site DNA #113.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, McNeil J;
XX DR WPI; 2000-086439/07.
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XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC internal loop region; (b) 2 nucleotides forming a first side of a second
XX CC double stranded (ds) region; (c) 4 nucleotides forming a first side of an
XX CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC ds region; (f) 4 or 5 nucleotides forming a second side of a first
XX CC internal loop region; (g) 3 nucleotides forming a second side of a second
XX CC internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUUAUCUUAAGCCUAGGGGC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUGUAGCCUAGGGGC 28
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Db 20 AAGATTCCTTTTGTAGCCCAAGGGC 46

RESULT 38
AAA71111
ID AAA71111 standard; RNA; 46 BP.
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AC AAA71111;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #187.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, McNeil J;
XX DR WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 122; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC internal loop region; (b) 2 nucleotides forming a first side of a second
XX CC double stranded (ds) region; (c) 4 nucleotides forming a first side of an
XX CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC ds region; (f) 4 or 5 nucleotides forming a second side of a first
XX CC internal loop region; (g) 3 nucleotides forming a second side of a second
XX CC internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUUAUCUUAAGCCUAGGGGC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 9 A; 11 C; 9 G; 0 T; 17 U; 0 Other;

Query Match 74.5%; Score 21.6; DB 3; Length 46;
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QY 1 UUAUUAUUUUUUUGUAGCCUAGGGGC 28
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Db 19 UUUUAUUUUUUUGUAGCCUAGGGGC 46

RESULT 39
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ID AAA71095 standard; DNA; 46 BP.
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XX AAA71095;

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XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site DNA #118.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 121; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
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XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
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XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUACUAGUUACAGAAAAC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 9 A; 11 C; 9 G; 17 T; 0 U; 0 Other;

Query Match 74.5%; Score 21.6; DB 3; Length 46;
Best Local Similarity 53.6%; Pred. No. 5, 7;
Matches 15; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

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Db 19 TTGTATCCTTCTGTAAAGCCCTACGGGC 46

RESULT 40
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ID AAA71109 standard; RNA; 46 BP.
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XX AC AAA71109;
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DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #185.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 122; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
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XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
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XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 9 A; 11 C; 9 G; 0 T; 17 U; 0 Other;

Query Match 74.5%; Score 21.6; DB 3; Length 46;
Best Local Similarity 85.7%; Pred. No. 5, 7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGUAGCCUAGGGGC 28
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Db 19 UUUGAUCCUUUCUGUAGCCUACGGGC 46

Search completed: April 18, 2004, 08:03:59
Job time : 205.667 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 08:41:44 ; Search time 159.667 Seconds
(without alignments)
812.711 Million cell updates/sec

Title: US-09-310-844C-23

Perfect score: 29

Sequence: 1 nmgauuununguaagccnangnm 29

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2890132 seqs, 223790429 residues

Total number of hits satisfying chosen parameters: 1657368

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	12.8	44.1	30	12	US-10-335-977-10024
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3	12.8	44.1	68	12	US-10-329-624-2762
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C 5	12.4	42.8	65	10	US-09-908-975-18725
6	12.2	42.1	50	15	US-10-131-827-454
7	12.2	42.1	60	10	US-09-908-975-9828
C 8	12.2	42.1	60	10	US-09-908-975-15109
9	12.2	42.1	60	10	US-09-908-975-18934
10	12.2	42.1	25	14	US-10-098-263B-76444
11	11.8	40.7	47	9	US-09-230-926A-35
12	11.8	40.7	60	10	US-09-908-975-15914
C 13	11.8	40.7	60	10	US-09-908-975-15914
14	11.8	40.7	60	10	US-09-908-975-17626
15	11.8	40.7	65	10	US-09-908-975-1254

65 10 US-09-908-975-30297
65 14 US-10-032-585-316
77 9 US-09-738-968-9
77 9 US-09-738-968-10
24 10 US-09-964-895-27
24 14 US-10-059-152-26
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31 10 US-09-817-879-6639
31 10 US-09-817-879-9154
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31 14 US-10-156-306-3281
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25 14 US-10-098-263B-37316
25 14 US-10-098-263B-100367
25 14 US-10-098-263B-129996
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33 12 US-10-150-407-29
33 15 US-10-346-880-29
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Sequence 30297, A
Sequence 316, App
Sequence 9, Appl
Sequence 10, Appl
Sequence 27, Appl
Sequence 26, Appl
Sequence 6917, Ap
Sequence 7188, Ap
Sequence 7495, Ap
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Sequence 1019, Ap
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Sequence 3281, Ap
Sequence 7, Appl
Sequence 15, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 5781, Ap
Sequence 12753, A
Sequence 14781, A
Sequence 24835, A
Sequence 23918, A
Sequence 279, App
Sequence 5191, Ap
Sequence 5192, Ap
Sequence 94421, A
Sequence 28, Appl
Sequence 28, Appl
Sequence 6202, Ap
Sequence 7920, Ap
Sequence 70533, A
Sequence 206, App
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Sequence 37316, A
Sequence 100367, A
Sequence 129996, A
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Sequence 2, Appl
Sequence 212, App
Sequence 275, App
Sequence 2842, Ap
Sequence 3942, Ap
Sequence 4871, Ap
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Sequence 7158, Ap
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Sequence 7531, Ap
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Sequence 6077, Ap
Sequence 19988, A
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C 108	10.8	37.2	25	12	US-10-675-685-1101	Sequence 1101, App	10.6	10.6	36.6	31	10	US-09-817-879-4986	Sequence 4986, App
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C 112	10.8	37.2	25	14	US-10-215-112-2121	Sequence 2121, App	10.6	10.6	36.6	31	10	US-09-817-879-7207	Sequence 7207, App
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C 122	10.8	37.2	45	10	US-09-993-345-130	Sequence 345, App	10.6	10.6	36.6	31	14	US-10-163-552-1089	Sequence 1089, App
C 123	10.8	37.2	45	10	US-09-993-345-342	Sequence 342, App	10.6	10.6	36.6	31	14	US-10-163-552-1254	Sequence 1254, App
C 124	10.8	37.2	47	15	US-10-349-143-2826	Sequence 2826, App	10.6	10.6	36.6	31	14	US-10-163-552-1525	Sequence 1525, App
C 125	10.8	37.2	47	15	US-10-349-143-3545	Sequence 3545, App	10.6	10.6	36.6	31	14	US-10-163-552-1528	Sequence 1528, App
C 126	10.8	37.2	50	14	US-09-993-346-343	Sequence 343, App	10.6	10.6	36.6	31	14	US-10-163-552-1790	Sequence 1790, App
C 127	10.8	37.2	50	14	US-10-073-118-22	Sequence 22, Appl	10.6	10.6	36.6	31	14	US-10-156-306-3240	Sequence 3240, App
C 128	10.8	37.2	50	14	US-10-334-729-44	Sequence 44, Appl	10.6	10.6	36.6	31	14	US-10-238-700-1481	Sequence 1481, App
C 129	10.8	37.2	50	15	US-10-131-827-117	Sequence 117, App	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 130	10.8	37.2	50	15	US-10-131-827-1489	Sequence 1489, App	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 131	10.8	37.2	50	15	US-10-131-827-2246	Sequence 2246, App	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 132	10.8	37.2	50	15	US-10-131-827-3662	Sequence 3662, App	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 133	10.8	37.2	51	10	US-09-951-061A-16	Sequence 16, Appl	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 134	10.8	37.2	51	12	US-10-441-788-16	Sequence 16, Appl	10.6	10.6	36.6	31	14	US-10-238-700-4018	Sequence 4018, App
C 135	10.8	37.2	51	14	US-10-267-384-16	Sequence 16, Appl	10.6	10.6	36.6	31	14	US-10-347-278-4	Sequence 4, Appl
C 136	10.8	37.2	60	10	US-09-908-975-5234	Sequence 5234, App	10.6	10.6	36.6	31	14	US-10-347-252-4	Sequence 4, Appl
C 137	10.8	37.2	60	10	US-09-908-975-9357	Sequence 9357, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 138	10.8	37.2	60	10	US-09-908-975-14519	Sequence 14519, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 139	10.8	37.2	60	10	US-09-908-975-14510	Sequence 14510, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 140	10.8	37.2	60	10	US-09-908-975-15340	Sequence 15340, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 141	10.8	37.2	60	10	US-09-908-975-18316	Sequence 18316, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 142	10.8	37.2	60	10	US-09-908-975-18316	Sequence 18316, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 143	10.8	37.2	60	10	US-09-908-975-20372	Sequence 20372, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 144	10.8	37.2	60	10	US-09-908-975-22793	Sequence 22793, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 145	10.8	37.2	60	10	US-09-908-975-23059	Sequence 23059, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 146	10.8	37.2	61	8	US-08-781-866A-1736	Sequence 1736, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 147	10.8	37.2	61	12	US-10-329-624-1736	Sequence 1736, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 148	10.8	37.2	65	10	US-09-908-975-29506	Sequence 29506, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 149	10.8	37.2	65	10	US-09-908-975-30019	Sequence 30019, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 150	10.8	37.2	65	10	US-09-908-975-30555	Sequence 30555, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 151	10.8	37.2	65	14	US-10-032-585-5000	Sequence 500, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 152	10.8	37.2	65	14	US-10-032-585-3201	Sequence 3201, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 153	10.8	37.2	65	14	US-10-032-585-3609	Sequence 3609, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 154	10.8	37.2	74	12	US-10-027-632-176850	Sequence 176850, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 155	10.8	37.2	74	12	US-10-027-632-176850	Sequence 176850, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 156	10.6	36.6	25	14	US-10-098-263B-1281	Sequence 1281, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 157	10.6	36.6	25	14	US-10-098-263B-1282	Sequence 1282, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 158	10.6	36.6	25	14	US-10-098-263B-32657	Sequence 32657, App	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 159	10.6	36.6	25	14	US-10-098-263B-71254	Sequence 71254, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 160	10.6	36.6	25	14	US-10-098-263B-95073	Sequence 95073, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl
C 161	10.6	36.6	25	14	US-10-098-263B-106778	Sequence 106778, A	10.6	10.6	36.6	31	14	US-10-116-519-18	Sequence 18, Appl

C 235	10.6	36.6	64	9	US-09-946-807-1311	Sequence 1311, Ap	308	10.4	35.9	60	10	US-09-908-975-22122	Sequence 22122, A
C 236	10.6	36.6	65	10	US-09-908-975-2126	Sequence 2126, Ap	C 309	10.4	35.9	60	10	US-09-908-975-22459	Sequence 22459, A
C 237	10.6	36.6	65	10	US-09-908-975-24310	Sequence 24310, A	C 310	10.4	35.9	60	10	US-09-908-975-31332	Sequence 31332, A
C 238	10.6	36.6	65	10	US-09-908-975-25756	Sequence 25756, A	C 311	10.4	35.9	60	12	US-10-609-217-415	Sequence 415, App
C 239	10.6	36.6	65	10	US-09-908-975-26141	Sequence 26141, A	C 312	10.4	35.9	60	12	US-10-632-388-415	Sequence 415, App
C 240	10.6	36.6	65	14	US-10-032-585-3015	Sequence 3015, Ap	C 313	10.4	35.9	60	12	US-10-632-388-415	Sequence 415, App
C 241	10.6	36.6	65	14	US-10-032-585-3752	Sequence 3752, Ap	C 314	10.4	35.9	61	12	US-10-609-217-400	Sequence 400, App
C 242	10.6	36.6	69	9	US-09-912-679-77	Sequence 77, Appl	C 315	10.4	35.9	61	12	US-10-632-388-400	Sequence 400, App
C 243	10.6	36.6	69	9	US-09-466-035-77	Sequence 77, Appl	C 316	10.4	35.9	61	12	US-10-651-723-400	Sequence 400, App
C 244	10.6	36.6	75	14	US-10-029-386-18583	Sequence 18583, A	C 317	10.4	35.9	64	12	US-10-027-632-58365	Sequence 58365, A
C 245	10.6	36.6	76	12	US-10-027-632-175644	Sequence 175644, A	C 318	10.4	35.9	64	15	US-10-027-632-58365	Sequence 58365, A
C 246	10.6	36.6	76	15	US-10-027-632-175644	Sequence 175644, A	C 319	10.4	35.9	65	10	US-09-908-975-1560	Sequence 1560, Ap
C 247	10.6	36.6	80	15	US-10-448-250-43	Sequence 43, Appl	C 320	10.4	35.9	65	10	US-09-908-975-1560	Sequence 1560, Ap
C 248	10.6	36.6	80	15	US-10-448-250-94	Sequence 94, Appl	C 321	10.4	35.9	65	10	US-09-908-975-27686	Sequence 27686, A
C 249	10.4	35.9	17	10	US-09-877-478-161	Sequence 161, App	C 322	10.4	35.9	65	12	US-10-027-632-52586	Sequence 52586, A
C 250	10.4	35.9	17	10	US-09-877-478-162	Sequence 162, App	C 323	10.4	35.9	71	14	US-10-223-666-242	Sequence 242, App
C 251	10.4	35.9	17	10	US-09-877-478-870	Sequence 870, App	C 324	10.4	35.9	77	12	US-10-027-632-52602	Sequence 52602, A
C 252	10.4	35.9	17	10	US-09-780-164-158	Sequence 158, App	C 325	10.4	35.9	77	15	US-10-027-632-52602	Sequence 52602, A
C 253	10.4	35.9	17	10	US-09-780-164-525	Sequence 525, App	C 326	10.2	35.2	77	15	US-10-027-632-52602	Sequence 52602, A
C 254	10.4	35.9	17	10	US-09-780-164-903	Sequence 903, App	C 327	10.2	35.2	20	12	US-09-771-357-60	Sequence 60, Appl
C 255	10.4	35.9	17	12	US-10-342-902-161	Sequence 161, App	C 328	10.2	35.2	20	12	US-10-160-786-38	Sequence 38, Appl
C 256	10.4	35.9	17	12	US-10-342-902-162	Sequence 162, App	C 329	10.2	35.2	20	14	US-10-059-579-60	Sequence 60, Appl
C 257	10.4	35.9	17	12	US-10-342-902-870	Sequence 870, App	C 330	10.2	35.2	20	14	US-10-160-632-51	Sequence 51, Appl
C 258	10.4	35.9	20	10	US-09-909-595-40	Sequence 40, Appl	C 331	10.2	35.2	20	15	US-10-300-683-259	Sequence 259, App
C 259	10.4	35.9	20	15	US-09-949-143-5557	Sequence 5557, Ap	C 332	10.2	35.2	21	9	US-09-984-186-20	Sequence 20, Appl
C 260	10.4	35.9	24	10	US-09-940-185-2196	Sequence 2196, Ap	C 333	10.2	35.2	21	14	US-10-237-667-20	Sequence 20, Appl
C 261	10.4	35.9	24	12	US-10-027-632-176342	Sequence 176342, A	C 334	10.2	35.2	21	14	US-10-237-708-20	Sequence 20, Appl
C 262	10.4	35.9	24	15	US-10-027-632-176342	Sequence 176342, A	C 335	10.2	35.2	21	14	US-10-237-708-20	Sequence 20, Appl
C 263	10.4	35.9	25	14	US-10-098-263B-10043	Sequence 10043, A	C 336	10.2	35.2	21	14	US-10-237-708-20	Sequence 20, Appl
C 264	10.4	35.9	25	14	US-10-098-263B-10044	Sequence 10044, A	C 337	10.2	35.2	21	14	US-10-237-708-20	Sequence 20, Appl
C 265	10.4	35.9	25	14	US-10-098-263B-12809	Sequence 12809, A	C 338	10.2	35.2	21	15	US-10-349-143-11708	Sequence 11708, A
C 266	10.4	35.9	25	14	US-10-098-263B-23797	Sequence 23797, A	C 339	10.2	35.2	22	14	US-10-315-1515-159	Sequence 159, App
C 267	10.4	35.9	25	14	US-10-098-263B-28307	Sequence 28307, A	C 340	10.2	35.2	22	15	US-10-015-115-193	Sequence 193, App
C 268	10.4	35.9	25	14	US-10-098-263B-49553	Sequence 49553, A	C 341	10.2	35.2	23	14	US-10-091-281-380	Sequence 380, App
C 269	10.4	35.9	25	14	US-10-098-263B-49554	Sequence 49554, A	C 342	10.2	35.2	23	9	US-09-897-798-18	Sequence 18, Appl
C 270	10.4	35.9	25	14	US-10-098-263B-66108	Sequence 66108, A	C 343	10.2	35.2	24	10	US-09-940-185-879	Sequence 879, App
C 271	10.4	35.9	25	14	US-10-098-263B-95040	Sequence 95040, A	C 344	10.2	35.2	24	14	US-10-174-513-18	Sequence 18, Appl
C 272	10.4	35.9	25	14	US-10-098-263B-95040	Sequence 95040, A	C 345	10.2	35.2	25	13	US-10-113-877-157	Sequence 157, App
C 273	10.4	35.9	29	9	US-09-925-664-77	Sequence 77, Appl	C 346	10.2	35.2	25	14	US-10-215-112-346	Sequence 346, App
C 274	10.4	35.9	30	9	US-09-770-517C-22	Sequence 22, Appl	C 347	10.2	35.2	25	14	US-10-215-112-6399	Sequence 6399, Ap
C 275	10.4	35.9	36	12	US-10-289-456-133	Sequence 133, App	C 348	10.2	35.2	25	14	US-10-215-112-8593	Sequence 8593, Ap
C 276	10.4	35.9	36	12	US-10-289-456-134	Sequence 134, App	C 349	10.2	35.2	25	14	US-10-098-263B-4175	Sequence 4175, Ap
C 277	10.4	35.9	36	14	US-10-289-456-360	Sequence 360, App	C 350	10.2	35.2	25	14	US-10-098-263B-4811	Sequence 4811, Ap
C 278	10.4	35.9	36	14	US-10-289-456-361	Sequence 361, App	C 351	10.2	35.2	25	14	US-10-098-263B-4811	Sequence 4811, Ap
C 279	10.4	35.9	36	15	US-10-346-190-140	Sequence 140, App	C 352	10.2	35.2	25	14	US-10-098-263B-7597	Sequence 7597, Ap
C 280	10.4	35.9	36	15	US-10-346-190-141	Sequence 141, App	C 353	10.2	35.2	25	14	US-10-098-263B-7598	Sequence 7598, Ap
C 281	10.4	35.9	38	12	US-09-877-478-4331	Sequence 4331, Ap	C 354	10.2	35.2	25	14	US-10-098-263B-16921	Sequence 16921, A
C 282	10.4	35.9	38	12	US-10-342-902-4331	Sequence 4331, Ap	C 355	10.2	35.2	25	14	US-10-098-263B-26350	Sequence 26350, A
C 283	10.4	35.9	41	15	US-10-167-634-60	Sequence 60, Appl	C 356	10.2	35.2	25	14	US-10-098-263B-39575	Sequence 39575, A
C 284	10.4	35.9	43	14	US-10-032-588-886	Sequence 886, App	C 357	10.2	35.2	25	14	US-10-098-263B-41638	Sequence 41638, A
C 285	10.4	35.9	47	12	US-10-333-429-156	Sequence 156, App	C 358	10.2	35.2	25	14	US-10-098-263B-59729	Sequence 59729, A
C 286	10.4	35.9	47	15	US-10-349-143-133	Sequence 133, App	C 359	10.2	35.2	25	14	US-10-098-263B-60056	Sequence 60056, A
C 287	10.4	35.9	47	15	US-10-349-143-430	Sequence 430, App	C 360	10.2	35.2	25	14	US-10-098-263B-61043	Sequence 61043, A
C 288	10.4	35.9	47	15	US-10-349-143-734	Sequence 734, App	C 361	10.2	35.2	25	14	US-10-098-263B-76443	Sequence 76443, A
C 289	10.4	35.9	47	15	US-10-349-143-2892	Sequence 2892, Ap	C 362	10.2	35.2	25	14	US-10-098-263B-80471	Sequence 80471, A
C 290	10.4	35.9	47	15	US-10-349-143-3619	Sequence 3619, Ap	C 363	10.2	35.2	25	14	US-10-098-263B-82295	Sequence 82295, A
C 291	10.4	35.9	49	9	US-09-962-537-47	Sequence 47, Appl	C 364	10.2	35.2	25	14	US-10-098-263B-88031	Sequence 88031, A
C 292	10.4	35.9	50	12	US-10-609-217-401	Sequence 401, App	C 365	10.2	35.2	25	14	US-10-098-263B-91814	Sequence 91814, A
C 293	10.4	35.9	50	12	US-10-632-388-401	Sequence 401, App	C 366	10.2	35.2	25	14	US-10-098-263B-96338	Sequence 96338, A
C 294	10.4	35.9	50	12	US-10-651-723-401	Sequence 401, App	C 367	10.2	35.2	25	14	US-10-098-263B-96488	Sequence 96488, A
C 295	10.4	35.9	50	15	US-10-131-827-2624	Sequence 2624, App	C 368	10.2	35.2	25	14	US-10-098-263B-110175	Sequence 110175, A
C 296	10.4	35.9	50	15	US-10-131-827-5493	Sequence 5493, Ap	C 369	10.2	35.2	25	14	US-10-098-263B-114655	Sequence 114655, A
C 297	10.4	35.9	57	12	US-10-609-217-414	Sequence 414, App	C 370	10.2	35.2	25	14	US-10-098-263B-117900	Sequence 117900, A
C 298	10.4	35.9	57	12	US-10-632-388-414	Sequence 414, App	C 371	10.2	35.2	25	14	US-10-098-263B-119104	Sequence 119104, A
C 299	10.4	35.9	57	12	US-10-651-723-414	Sequence 414, App	C 372	10.2	35.2	25	14	US-10-098-263B-127942	Sequence 127942, A
C 300	10.4	35.9	60	10	US-09-908-975-5937	Sequence 5937, Ap	C 373	10.2	35.2	25	14	US-10-098-263B-128239	Sequence 128239, A
C 301	10.4	35.9	60	10	US-09-908-975-10589	Sequence 10589, A	C 374	10.2	35.2	25	14	US-10-098-263B-128695	Sequence 128695, A
C 302	10.4	35.9	60	10	US-09-908-975-12876	Sequence 12876, A	C 375	10.2	35.2	26	14	US-10-164-776-14	Sequence 14, Appl
C 303	10.4	35.9	60	10	US-09-908-975-16138	Sequence 16138, A	C 376	10.2	35.2	27	14	US-10-005-956-1305	Sequence 1305, Ap
C 304	10.4	35.9	60	10	US-09-908-975-16164	Sequence 16164, A	C 377	10.2	35.2	29	15	US-10-369-214-98	Sequence 98, Appl
C 305	10.4	35.9	60	10	US-09-908-975-19865	Sequence 19865, A	C 378	10.2	35.2	30	12	US-10-338-674-2769	Sequence 2769, Ap
C 306	10.4	35.9	60	10	US-09-908-975-20463	Sequence 20463, A	C 379	10.2	35.2	30	12	US-10-339-674-2770	Sequence 2770, Ap
C 307	10.4	35.9	60	10	US-09-908-975-21901	Sequence 21901, A	C 380	10.2	35.2	30	14	US-10-436-523-773	Sequence 773, Appl

C 381	10.2	35.2	31	9	US-09-745-008-7	Sequence 7, Appli	C 454	10.2	35.2	60	15	US-10-360-828-6	Sequence 6, Appli
C 382	10.2	35.2	32	12	US-10-371-771-16	Sequence 16, Appli	C 455	10.2	35.2	62	15	US-10-387-387-1	Sequence 1, Appli
C 383	10.2	35.2	33	9	US-09-875-494-22	Sequence 22, Appli	C 456	10.2	35.2	64	8	US-08-825-486-38	Sequence 38, Appli
C 384	10.2	35.2	33	14	US-10-214-419-6	Sequence 6, Appli	C 457	10.2	35.2	64	9	US-09-372-044-38	Sequence 38, Appli
C 385	10.2	35.2	36	14	US-10-022-832-73	Sequence 73, Appli	C 458	10.2	35.2	64	9	US-09-924-417-46	Sequence 46, Appli
C 386	10.2	35.2	40	9	US-09-738-968-34	Sequence 34, Appli	C 459	10.2	35.2	65	10	US-09-908-975-732	Sequence 732, App
C 387	10.2	35.2	40	10	US-09-963-827B-173	Sequence 173, App	C 460	10.2	35.2	65	10	US-09-908-975-990	Sequence 990, App
C 388	10.2	35.2	40	12	US-10-339-674-2728	Sequence 2728, App	C 461	10.2	35.2	65	10	US-09-908-975-1265	Sequence 1265, App
C 389	10.2	35.2	41	12	US-10-453-827-162	Sequence 162, App	C 462	10.2	35.2	65	10	US-09-908-975-1535	Sequence 1535, App
C 390	10.2	35.2	42	13	US-10-077-480-5	Sequence 5, Appli	C 463	10.2	35.2	65	10	US-09-908-975-2183	Sequence 2183, App
C 391	10.2	35.2	44	14	US-10-085-797-17	Sequence 17, Appli	C 464	10.2	35.2	65	10	US-09-908-975-2624	Sequence 2624, App
C 392	10.2	35.2	45	9	US-09-943-722-86	Sequence 86, Appli	C 465	10.2	35.2	65	10	US-09-908-975-3035	Sequence 3035, App
C 393	10.2	35.2	46	14	US-10-198-235-125	Sequence 125, App	C 466	10.2	35.2	65	10	US-09-908-975-3545	Sequence 3545, App
C 394	10.2	35.2	47	9	US-09-230-926A-50	Sequence 50, Appli	C 467	10.2	35.2	65	10	US-09-908-975-3975	Sequence 3975, App
C 395	10.2	35.2	47	12	US-10-339-674-3443	Sequence 3443, App	C 468	10.2	35.2	65	10	US-09-908-975-24232	Sequence 24232, A
C 396	10.2	35.2	47	15	US-10-349-143-686	Sequence 866, App	C 469	10.2	35.2	65	10	US-09-908-975-24939	Sequence 24939, A
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C 412	10.2	35.2	52	12	US-10-339-674-2771	Sequence 2771, App	C 485	10.2	35.2	71	12	US-10-339-674-947	Sequence 947, App
C 413	10.2	35.2	56	12	US-10-339-674-3441	Sequence 3441, App	C 486	10.2	35.2	71	14	US-10-066-960-108	Sequence 108, App
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C 415	10.2	35.2	57	12	US-10-339-674-2764	Sequence 2764, App	C 488	10.2	35.2	72	12	US-10-339-674-2730	Sequence 2730, App
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C 423	10.2	35.2	60	10	US-09-908-975-5646	Sequence 5646, App	C 496	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
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C 432	10.2	35.2	60	10	US-09-908-975-13840	Sequence 13840, A	C 505	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
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C 435	10.2	35.2	60	10	US-09-908-975-15324	Sequence 15324, A	C 508	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
C 436	10.2	35.2	60	10	US-09-908-975-15514	Sequence 15514, A	C 509	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
C 437	10.2	35.2	60	10	US-09-908-975-16347	Sequence 16347, A	C 510	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
C 438	10.2	35.2	60	10	US-09-908-975-16753	Sequence 16753, A	C 511	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
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C 442	10.2	35.2	60	10	US-09-908-975-20345	Sequence 20345, A	C 515	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
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C 448	10.2	35.2	60	12	US-10-329-624-3478	Sequence 3478, App	C 521	10.2	35.2	80	14	US-10-423-495-32	Sequence 32, Appli
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597	10	34.5	25	11	US-09-904-805-321	Sequence 321, App	C 670	10	34.5	31	10	US-09-848-754A-6940	Sequence 6940, App
598	10	34.5	25	11	US-09-904-938A-321	Sequence 321, App	C 671	10	34.5	31	10	US-09-848-754A-6940	Sequence 6940, App
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C 684	10	34.5	31	10	US-09-930-423-3558	Sequence 3558, Ap	C 757	10	34.5	31	10	US-09-817-879-7114	Sequence 7114, Ap
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C 698	10	34.5	31	10	US-09-740-332-6200	Sequence 6200, Ap	C 771	10	34.5	31	10	US-09-817-879-9111	Sequence 9111, Ap
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C 702	10	34.5	31	10	US-09-740-332-6847	Sequence 6847, Ap	C 775	10	34.5	31	10	US-09-817-879-9228	Sequence 9228, Ap
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C 727	10	34.5	31	10	US-09-740-332-9228	Sequence 9228, Ap	C 800	10	34.5	31	14	US-10-156-306-2923	Sequence 3283, Ap
C 728	10	34.5	31	10	US-09-740-332-9258	Sequence 9258, Ap	C 801	10	34.5	31	14	US-10-156-306-3070	Sequence 3283, Ap
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C 733	10	34.5	31	10	US-09-745-237A-3522	Sequence 3522, Ap	C 806	10	34.5	31	14	US-10-156-306-6443	Sequence 6443, Ap
C 734	10	34.5	31	10	US-09-745-237A-3523	Sequence 3523, Ap	C 807	10	34.5	31	14	US-10-156-306-6448	Sequence 6448, Ap
C 735	10	34.5	31	10	US-09-745-237A-3530	Sequence 3530, Ap	C 808	10	34.5	31	14	US-10-156-306-6452	Sequence 6452, Ap
C 736	10	34.5	31	10	US-09-745-237A-3636	Sequence 3636, Ap	C 809	10	34.5	31	14	US-10-156-306-6458	Sequence 6516, Ap
C 737	10	34.5	31	10	US-09-817-879-4873	Sequence 4873, Ap	C 810	10	34.5	31	14	US-10-156-306-6511	Sequence 6511, Ap
C 738	10	34.5	31	10	US-09-817-879-5006	Sequence 5006, Ap	C 811	10	34.5	31	14	US-10-156-306-6516	Sequence 6516, Ap
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C 744	10	34.5	31	10	US-09-817-879-5871	Sequence 5871, Ap	C 817	10	34.5	31	14	US-10-238-700-1349	Sequence 1349, Ap
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C 820	10	34.5	31	14	US-10-238-700-2415	Sequence 2415, Ap	893	10	34.5	63	12	US-10-027-632-176912	Sequence 176912,
C 821	10	34.5	31	14	US-10-238-700-3677	Sequence 3677, Ap	894	10	34.5	63	15	US-10-027-632-176912	Sequence 176912,
C 822	10	34.5	31	14	US-10-238-700-3761	Sequence 3761, Ap	895	10	34.5	65	10	US-09-908-975-156	Sequence 156, App
C 823	10	34.5	31	14	US-10-238-700-3777	Sequence 3777, Ap	896	10	34.5	65	10	US-09-908-975-2136	Sequence 2136, Ap
C 824	10	34.5	31	14	US-10-238-700-3845	Sequence 3845, Ap	897	10	34.5	65	10	US-09-908-975-2596	Sequence 2596, Ap
C 825	10	34.5	31	14	US-10-238-700-3965	Sequence 3965, Ap	898	10	34.5	65	10	US-09-908-975-3442	Sequence 3442, Ap
C 826	10	34.5	31	14	US-10-238-700-3967	Sequence 3967, Ap	899	10	34.5	65	10	US-09-908-975-4004	Sequence 4004, Ap
C 827	10	34.5	31	14	US-10-238-700-4059	Sequence 4059, Ap	900	10	34.5	65	10	US-09-908-975-2390	Sequence 2390, A
C 828	10	34.5	31	14	US-10-238-700-4435	Sequence 4435, Ap	901	10	34.5	65	10	US-09-908-975-2390	Sequence 2390, A
C 829	10	34.5	31	14	US-10-238-700-4541	Sequence 4541, Ap	902	10	34.5	65	10	US-09-908-975-25500	Sequence 25500, A
C 830	10	34.5	31	14	US-10-238-700-4552	Sequence 4552, Ap	903	10	34.5	65	10	US-09-908-975-25539	Sequence 25539, A
C 831	10	34.5	31	14	US-10-230-006-1725	Sequence 1725, Ap	904	10	34.5	65	10	US-09-908-975-26289	Sequence 26289, A
C 832	10	34.5	31	14	US-10-230-006-1740	Sequence 1740, Ap	905	10	34.5	65	10	US-09-908-975-26414	Sequence 26414, A
C 833	10	34.5	31	14	US-10-230-006-1767	Sequence 1767, Ap	906	10	34.5	65	10	US-09-908-975-27440	Sequence 27440, A
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C 835	10	34.5	31	14	US-10-230-006-1972	Sequence 1972, Ap	908	10	34.5	65	10	US-09-908-975-28083	Sequence 28083, A
C 836	10	34.5	31	14	US-10-230-006-2011	Sequence 2011, Ap	909	10	34.5	65	10	US-09-908-975-29336	Sequence 29336, A
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C 838	10	34.5	33	14	US-10-389-177-7	Sequence 7, Appli	911	10	34.5	65	10	US-09-908-975-30118	Sequence 30118, A
C 839	10	34.5	33	15	US-10-360-828-56	Sequence 56, Appl	912	10	34.5	65	14	US-10-313-542-258	Sequence 258, App
C 840	10	34.5	35	10	US-09-365-940-19	Sequence 19, Appl	913	10	34.5	65	14	US-10-032-585-136	Sequence 136, App
C 841	10	34.5	35	14	US-10-200-242-19	Sequence 19, Appl	914	10	34.5	65	14	US-10-032-585-433	Sequence 433, App
C 842	10	34.5	35	15	US-10-147-603-53	Sequence 53, Appl	915	10	34.5	65	14	US-10-032-585-463	Sequence 463, App
C 843	10	34.5	35	15	US-10-200-242-19	Sequence 19, Appl	916	10	34.5	65	14	US-10-032-585-3405	Sequence 3405, Ap
C 844	10	34.5	35	15	US-10-420-194-658	Sequence 658, App	917	10	34.5	72	14	US-10-204-884-131	Sequence 131, App
C 845	10	34.5	37	9	US-09-924-154-9	Sequence 9, Appli	918	10	34.5	72	14	US-10-029-386-15365	Sequence 15365, A
C 846	10	34.5	38	11	US-09-405-032-66	Sequence 66, Appl	919	10	34.5	80	14	US-10-029-386-14002	Sequence 14002, A
C 847	10	34.5	39	9	US-09-894-633A-39	Sequence 39, Appl	920	10	34.5	80	15	US-10-448-250-21	Sequence 21, Appl
C 848	10	34.5	40	15	US-10-411-066-121	Sequence 121, App	921	9.8	33.8	17	9	US-09-866-108-10208	Sequence 10208, A
C 849	10	34.5	41	12	US-10-453-827-99	Sequence 99, Appl	922	9.8	33.8	17	9	US-09-866-108-10209	Sequence 10209, A
C 850	10	34.5	41	12	US-10-339-674-46	Sequence 46, Appl	923	9.8	33.8	17	9	US-09-827-998-281	Sequence 281, App
C 851	10	34.5	41	12	US-10-339-674-47	Sequence 47, Appl	924	9.8	33.8	17	9	US-09-827-998-282	Sequence 282, App
C 852	10	34.5	42	13	US-10-339-674-45	Sequence 45, Appl	925	9.8	33.8	17	9	US-09-827-998-283	Sequence 283, App
C 853	10	34.5	42	13	US-10-025-367-15	Sequence 15, Appl	926	9.8	33.8	17	9	US-09-969-373-4322	Sequence 4322, Ap
C 854	10	34.5	42	14	US-10-186-867-16	Sequence 16, Appl	927	9.8	33.8	17	10	US-09-877-478-163	Sequence 163, App
C 855	10	34.5	42	14	US-10-400-377-39	Sequence 39, Appl	928	9.8	33.8	17	10	US-09-877-478-1470	Sequence 1470, Ap
C 856	10	34.5	42	14	US-10-400-708-39	Sequence 39, Appl	929	9.8	33.8	17	12	US-10-342-902-163	Sequence 163, App
C 857	10	34.5	42	14	US-10-298-148-39	Sequence 39, Appl	930	9.8	33.8	17	12	US-10-342-902-1470	Sequence 1470, Ap
C 858	10	34.5	45	12	US-10-278-768-28	Sequence 28, Appl	931	9.8	33.8	17	12	US-10-675-685-281	Sequence 281, App
C 859	10	34.5	45	14	US-10-151-716-11	Sequence 11, Appl	932	9.8	33.8	17	12	US-10-675-685-282	Sequence 282, App
C 860	10	34.5	45	9	US-09-978-274A-22	Sequence 22, Appl	933	9.8	33.8	17	14	US-10-675-685-283	Sequence 283, App
C 861	10	34.5	47	14	US-10-263-103-6	Sequence 6, Appli	934	9.8	33.8	17	14	US-10-339-793-396	Sequence 396, App
C 862	10	34.5	47	14	US-10-263-103-7	Sequence 7, Appli	935	9.8	33.8	18	15	US-10-349-143-5466	Sequence 5466, Ap
C 863	10	34.5	47	15	US-10-349-143-1676	Sequence 1676, Ap	936	9.8	33.8	18	15	US-10-349-143-7686	Sequence 7686, Ap
C 864	10	34.5	47	15	US-10-349-143-2668	Sequence 2668, Ap	937	9.8	33.8	19	10	US-09-911-226-7	Sequence 7, Appli
C 865	10	34.5	47	15	US-10-349-143-2903	Sequence 2903, Ap	938	9.8	33.8	19	12	US-10-700-018-7	Sequence 7, Appli
C 866	10	34.5	49	8	US-09-962-537-46	Sequence 46, Appl	939	9.8	33.8	19	15	US-10-349-143-4780	Sequence 4780, Ap
C 867	10	34.5	50	8	US-08-781-986A-2247	Sequence 2247, Ap	940	9.8	33.8	19	15	US-10-349-143-5884	Sequence 5884, Ap
C 868	10	34.5	50	12	US-10-329-624-2247	Sequence 2247, Ap	941	9.8	33.8	20	12	US-10-376-523-69	Sequence 69, Appl
C 869	10	34.5	50	15	US-10-131-827-6087	Sequence 6087, Ap	942	9.8	33.8	20	14	US-10-012-984-44	Sequence 44, Appl
C 870	10	34.5	50	15	US-10-131-827-7657	Sequence 7657, Ap	943	9.8	33.8	20	14	US-10-008-789-78	Sequence 78, Appl
C 871	10	34.5	52	12	US-10-027-632-176418	Sequence 176418, Ap	944	9.8	33.8	20	14	US-10-279-964-3	Sequence 3, Appli
C 872	10	34.5	52	15	US-10-027-632-176418	Sequence 176418, Ap	945	9.8	33.8	20	15	US-10-289-762-3600	Sequence 3600, Ap
C 873	10	34.5	53	10	US-09-918-156-62	Sequence 62, Appl	946	9.8	33.8	20	15	US-10-138-588-159	Sequence 159, App
C 874	10	34.5	60	10	US-09-918-740-30	Sequence 30, Appl	947	9.8	33.8	20	16	US-10-210-429-45	Sequence 45, Appl
C 875	10	34.5	60	10	US-09-908-975-8204	Sequence 8204, Ap	948	9.8	33.8	20	16	US-10-210-429-116	Sequence 116, App
C 876	10	34.5	60	10	US-09-908-975-9728	Sequence 9728, Ap	949	9.8	33.8	21	9	US-09-765-081-363	Sequence 363, App
C 877	10	34.5	60	10	US-09-908-975-9757	Sequence 9757, Ap	950	9.8	33.8	21	9	US-09-815-156-4	Sequence 4, Appli
C 878	10	34.5	60	10	US-09-908-975-13703	Sequence 13703, A	951	9.8	33.8	21	10	US-09-229-751A-2	Sequence 2, Appli
C 879	10	34.5	60	10	US-09-908-975-14132	Sequence 14132, A	952	9.8	33.8	21	10	US-09-988-626-153	Sequence 153, App
C 880	10	34.5	60	10	US-09-908-975-14399	Sequence 14399, A	953	9.8	33.8	21	10	US-09-988-687-153	Sequence 153, App
C 881	10	34.5	60	10	US-09-908-975-14420	Sequence 14420, A	954	9.8	33.8	21	10	US-09-988-686-153	Sequence 153, App
C 882	10	34.5	60	10	US-09-908-975-15007	Sequence 15007, A	955	9.8	33.8	21	13	US-10-075-425-3	Sequence 3, Appli
C 883	10	34.5	60	10	US-09-908-975-15248	Sequence 15248, A	956	9.8	33.8	22	9	US-09-870-745-9	Sequence 9, Appli
C 884	10	34.5	60	10	US-09-908-975-18236	Sequence 18236, A	957	9.8	33.8	22	9	US-09-810-993-6	Sequence 6, Appli
C 885	10	34.5	60	10	US-09-908-975-20732	Sequence 20732, A	958	9.8	33.8	22	9	US-09-810-993-19	Sequence 19, Appl
C 886	10	34.5	60	10	US-09-908-975-20766	Sequence 20766, A	959	9.8	33.8	22	14	US-10-151-484-27	Sequence 27, Appl
C 887	10	34.5	60	13	US-09-908-975-21435	Sequence 21435, A	960	9.8	33.8	22	14	US-10-251-210-6	Sequence 19, Appl
C 888	10	34.5	60	14	US-10-025-367-19	Sequence 19, Appl	961	9.8	33.8	22	14	US-10-251-210-19	Sequence 19, Appl
C 889	10	34.5	60	14	US-10-099-382-6	Sequence 6, Appli	962	9.8	33.8	22	14	US-10-294-249-34	Sequence 34, Appl
C 890	10	34.5	60	14	US-10-099-382-7	Sequence 7, Appli	963	9.8	33.8	23	13	US-10-147-391-22	Sequence 22, Appl
C 891	10	34.5	61	14	US-10-349-508-66	Sequence 66, Appl	964	9.8	33.8	23	14	US-10-241-332-22	Sequence 22, Appl


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Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANG 25
   |||:|:|:|:|:|:|
Db 3 ATCTGTTCCTAAGCCGACG 23

RESULT 3
US-10-329-624-2762
; Sequence 2762, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2762:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

US-10-329-624-2762
Query Match 44.1%; Score 12.8; DB 12; Length 68;
Best Local Similarity 47.6%; Pred. No. 2.6e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANG 25
   |||:|:|:|:|:|:|
Db 3 ATCTGTTCCTAAGCCGACG 23

RESULT 4
US-09-908-975-18725/c
; Sequence 18725, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
```

```
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18725
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18725

Query Match 42.8%; Score 12.4; DB 10; Length 60;
Best Local Similarity 55.6%; Pred. No. 4.4e+03;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 CUUUNNGUAGCCCNANG 25
   |||:|:|:|:|:|:|
Db 25 CTTTCTGAAGCCCATG 8

RESULT 5
US-09-908-975-2848/c
; Sequence 2848, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2848
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-2848

Query Match 42.8%; Score 12.4; DB 10; Length 65;
Best Local Similarity 52.9%; Pred. No. 4.4e+03;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGGCC 20
   |||:|:|:|:|:|:|
Db 53 GATACTTCAGTAAGCC 37

RESULT 6
US-10-131-827-464
; Sequence 464, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
```



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; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661300120
; CURRENT APPLICATION NUMBER: US/10/131.827
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 464
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-464

Query Match      42.1%; Score 12.2; DB 15; Length 50;
Best Local Similarity 45.5%; Pred. No. 5.5e+03;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||:::|||||
Db      22 GAGGCTTTCTAAGCCCAAG 43

RESULT 7
US-09-908-975-9828
; Sequence 9828, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9828
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-9828

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 52.8%; Pred. No. 5.7e+03;
Matches 12; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY      5 AUNCUUNNGUAGCCCNANG 27
      |||:::|||||
Db      34 AACCTCATGTAAGCCCAAGTG 56

RESULT 8
US-09-908-975-12187/c
; Sequence 12187, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat

```

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; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 12187
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12187

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 40.9%; Pred. No. 5.7e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||:::|||||
Db      54 GATTCTTCTAGCGCGTAAG 33

RESULT 9
US-09-908-975-15109/c
; Sequence 15109, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15109
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15109

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 45.5%; Pred. No. 5.7e+03;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||:::|||||
Db      37 GATGCTTCTGATGGCCAAG 16

RESULT 10
US-09-908-975-18934
; Sequence 18934, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon

```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18934
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18934

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 43.5%; Pred. No. 5.7e+03;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      5 AUNCUUNNGUAGCCCNANGNG 27
       |: : : |: : |: : |: : |: : |: :
DB      27 ATCCGTTGCGTARGCAGAGAG 49

RESULT 11
US-10-098-263B-76444
; Sequence 76444, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-76444

Query Match      40.7%; Score 11.8; DB 14; Length 25;
Best Local Similarity 44.4%; Pred. No. 8.4e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCC 21
       |: : : |: : |: : |: :
DB      1 GATACCTTTTAAAGTCC 18

RESULT 12
US-09-230-926A-35
; Sequence 35, Application US/09230926A
; Patent No. US20020168633A1
; GENERAL INFORMATION:
; APPLICANT: MABILIAT, Claude
; APPLICANT: SCHLEIFER, Karl-Heinz
; APPLICANT: LUDWIG, Wolfgang
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 23S RNA OF BACTERIA OF THE GENUS CHLAMYDIA
; TITLE OF INVENTION: USE AS A PROBE, PRIMER, AND IN A REAGENT AND A DETECTION PROCEDURE
; FILE REFERENCE: 102682
; CURRENT APPLICATION NUMBER: US/09/230,926A
; CURRENT FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01157
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: FR 97/07200
; PRIOR FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Chlamydia pneumoniae
US-09-230-926A-35

Query Match      40.7%; Score 11.8; DB 9; Length 47;
Best Local Similarity 65.0%; Pred. No. 9.3e+03;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 UNCUCUUNGUAGCCCNANG 25
       |: : : |: : |: : |: : |: :
DB      28 UCCUCGCGUAGGCCAAGG 47

RESULT 13
US-09-908-975-15914/c
; Sequence 15914, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15914
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15914

Query Match      40.7%; Score 11.8; DB 10; Length 60;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCC 21
       |: : : |: : |: : |: :
DB      30 GAGCGTTTGAGTGAGCCC 13

RESULT 14
US-09-908-975-17626
; Sequence 17626, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 17626
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-17626

Query Match          40.7%; Score 11.8; DB 10; Length 60;
Best Local Similarity 40.0%; Pred. No. 9.7e+03;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      6 UNCUUNNGUAGCCCNANG 25
      : : : : :
Db      28 TGCCTTTGGTAAGCACTTGG 47

RESULT 15
US-09-908-975-1254
; Sequence 1254, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1254
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-1254

Query Match          40.7%; Score 11.8; DB 10; Length 65;
Best Local Similarity 45.0%; Pred. No. 9.8e+03;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      6 UNCUUNNGUAGCCCNANG 25
      : : : : :
Db      11 TGCCTTTGGTAAGTCCAGG 30

RESULT 16
US-09-908-975-30297
; Sequence 30297, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30297
```

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; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-30297

Query Match          40.7%; Score 11.8; DB 10; Length 65;
Best Local Similarity 50.0%; Pred. No. 9.8e+03;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGGCC 21
      : : : : :
Db      37 GATTCCTTCCCAAGCCC 54

RESULT 17
US-10-032-585-316
; Sequence 316, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-316

Query Match          40.7%; Score 11.8; DB 14; Length 65;
Best Local Similarity 42.1%; Pred. No. 9.8e+03;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      5 AUNCUUNNGUAGCCCNAA 23
      : : : : :
Db      14 ATACTTCAGTATATACCAA 32

RESULT 18
US-09-738-968-9/c
; Sequence 9, Application US/09738968
; Patent No. US20010037016A1
; GENERAL INFORMATION:
; APPLICANT: Contag, Pamela R.
; APPLICANT: Purchio, Anthony
; APPLICANT: Zhang, Ning
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS
; TITLE OF INVENTION: MODULATING COMPOUNDS
; FILE REFERENCE: 9400-0012.20
; CURRENT APPLICATION NUMBER: US/09/738,968
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/465,978
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer F3R31
US-09-738-968-9

Query Match          40.7%; Score 11.8; DB 9; Length 77;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

QY 4 GAUNCUUNNGUAGAGCC 21
||: ||: :|||
Db 23 GATGCAATTAATTAAGCC 6

RESULT 19

US-09-738-968-10
; Sequence 10, Application US/09738968
; Patent No. US20010037016A1
; GENERAL INFORMATION:
; APPLICANT: Contag, Pamela R.
; APPLICANT: Purchio, Anthony
; APPLICANT: Zhang, Ning

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS

; FILE REFERENCE: 9400-0012.20

; CURRENT APPLICATION NUMBER: US/09/738,968

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 09/465,978

; PRIOR FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 10

; LENGTH: 77

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer P3R32

US-09-738-968-10

Query Match 40.7%; Score 11.8; DB 9; Length 77;

Best Local Similarity 50.0%; Pred. No. 1e+04;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCC 21
||: ||: :|||
Db 59 GATGCAATTAATTAAGCC 76

RESULT 20

US-09-964-895-27
; Sequence 27, Application US/09964895
; Publication No. US20030099667A1

; GENERAL INFORMATION:

; APPLICANT: Zeon Corporation

; TITLE OF INVENTION: Avian herpesvirus-based recombinant Gumboro disease

; FILE REFERENCE: ZHT/1BD-E

; CURRENT APPLICATION NUMBER: US/09/964,895

; CURRENT FILING DATE: 2001-09-28

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Gallid herpesvirus 2

US-09-964-895-27

Query Match 40.0%; Score 11.6; DB 10; Length 24;

Best Local Similarity 45.8%; Pred. No. 1.1e+04;

Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCCNANGNG 27
||: ||: :|||
Db 1 GGTGCAATTCGTAAGACCGATGG 24

RESULT 21

US-10-059-152-26
; Sequence 26, Application US/10059152
; Publication No. US20030157703A1

; GENERAL INFORMATION:

; APPLICANT: Zeon Corporation

; TITLE OF INVENTION: Recombinant herpesvirus of turkeys and use thereof

; FILE REFERENCE: NDV

; CURRENT APPLICATION NUMBER: US/10/059,152

; CURRENT FILING DATE: 2001-01-31

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-152-26

Query Match 40.0%; Score 11.6; DB 14; Length 24;

Best Local Similarity 45.8%; Pred. No. 1.1e+04;

Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCCNANGNG 27
||: ||: :|||
Db 1 GGTGCAATTCGTAAGACCGATGG 24

RESULT 22

US-09-848-754A-6937/c

; Sequence 6937, Application US/09848754A

; Publication No. US20030073207A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

; FILE REFERENCE: MBH00-958-1 (400/018)

; CURRENT APPLICATION NUMBER: US/09/848,754A

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 9645

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6937

; LENGTH: 31

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-6937

Query Match 40.0%; Score 11.6; DB 10; Length 31;

Best Local Similarity 45.8%; Pred. No. 1.1e+04;

Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCCNANGNG 27
||: ||: :|||
Db 25 GATCGTTGTAGCTAGCCCAAGGG 2

RESULT 23

US-09-848-754A-7188/c

; Sequence 7188, Application US/09848754A

; Publication No. US20030073207A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

; FILE REFERENCE: MBH00-958-1 (400/018)

; CURRENT APPLICATION NUMBER: US/09/848,754A

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 9645

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7188

; LENGTH: 31

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid

US-09-848-754A-7188

Query Match 40.0%; Score 11.6; DB 10; Length 24;

Best Local Similarity 45.8%; Pred. No. 1.1e+04;

Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCCNANGNG 27
||: ||: :|||
Db 1 GGTGCAATTCGTAAGACCGATGG 24

Query Match	40.0%;	Score 11.6;	DB 10;	Length 31;
Best Local Similarity	45.8%;	Pred. No. 1.1e+04;		
Matches 11;	Conservative	3;	Mismatches 10;	Indels 0;
Gaps 0;				
Qy	4	GAUNCUUNNGUAGCCCNANGNG	27	
		: :		
ph	25	GATCGTTGTAGCTAGCCCGAAGAG	2	

RESULT 28
US-09-817-879-9154/c
; Sequence 9154, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F

Db 8 GTGTCTCTGGTAAAGTCGACGAG 31

RESULT 33

US-09-800-130A-8/c
; Sequence 8, Application US/09800130A
; Publication No. US20030188346A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; FILE REFERENCE: 60/188,093
; CURRENT APPLICATION NUMBER: US/09/800,130A
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(56)
; OTHER INFORMATION: fully synthetic DNA leader sequence
US-09-800-130A-8

Query Match 40.0%; Score 11.6; DB 10; Length 56;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAAGCCCNANGNG 27

Db 28 GCCTTAATTAATTAAGCCCTAGGAG 5

RESULT 34

US-10-413-909-8/c
; Sequence 8, Application US/10413909
; Publication No. US20030192072A1
; GENERAL INFORMATION:
; APPLICANT: Baerson, Scott
; APPLICANT: Heck, Gregory
; APPLICANT: Rodriguez, Damian
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions
; FILE REFERENCE: 11898.0019.00DVUS01 (WOBS019--1)
; CURRENT APPLICATION NUMBER: US/10/413,909
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/188,093
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: fully synthetic DNA leader sequence
; NAME/KEY: 5'UTR
; LOCATION: (1)..(56)
; OTHER INFORMATION: fully synthetic DNA leader sequence
US-10-413-909-8

Query Match 40.0%; Score 11.6; DB 14; Length 56;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAAGCCCNANGNG 27

Db 28 GCCTTAATTAATTAAGCCCTAGGAG 5

RESULT 35

US-09-908-975-5781
; Sequence 5781, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5781
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-5781

Query Match 40.0%; Score 11.6; DB 10; Length 60;

Best Local Similarity 50.0%; Pred. No. 1.3e+04;

Matches 12; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAAGCCCNANGNG 27

Db 7 GAGCTTGTACGGAAGCCCTATGTG 30

RESULT 36

US-09-908-975-12753/c
; Sequence 12753, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12753
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12753

Query Match 40.0%; Score 11.6; DB 10; Length 60;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;

Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAAGCCCNANGNG 27

Db 46 GGTTCCTCTGGGTAGGCGCAATGTG 23

US-09-908-975-29918
; Sequence 29918, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; CURRENT APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29918
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-29918
Query Match 40.0%; Score 11.6; DB 10; Length 65;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAAGCCCNANGNG 27
DB 30 GATCCTGAAGCAAGCCCAAGAG 53
RESULT 40
US-10-435-696-279
; Sequence 279, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSI
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 279
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D17S1955 forward primer
US-10-435-696-279
Query Match 39.3%; Score 11.4; DB 15; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.4e+04;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 10 UUNNGUAAGCCCNANGNG 27
DB 3 TAATGTAAGCCCATGAG 20
Search completed: April 18, 2004, 11:55:16
Job time : 172.667 secs

US-09-908-975-14781/c
; Sequence 14781, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT FILING DATE: 2001-07-20
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14781
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14781
Query Match 40.0%; Score 11.6; DB 10; Length 60;
Best Local Similarity 41.7%; Pred. No. 1.3e+04;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAAGCCCNANGNG 27
DB 45 GACTCTTGGTTAAGCCCTCCTGAG 22
RESULT 38
US-09-908-975-24835
; Sequence 24835, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24835
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-24835
Query Match 40.0%; Score 11.6; DB 10; Length 65;
Best Local Similarity 41.7%; Pred. No. 1.3e+04;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 4 GAUNCUUNNGUAAGCCCNANGNG 27
DB 5 GATGGGTCAGTAATGCCCAGGAG 28
RESULT 39

us-09-310-844c-23.max.rnpb

Tue Apr 20 10:03:02 2004

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:34:53 ; Search time 36.6667 Seconds
(without alignments)
438.916 Million cell updates/sec

Title: US-09-310-844C-23

Perfect score: 29

Sequence: 1 nngauncuunnguaagccnangnrr. 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 915622

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.8	44.1	68	4	US-08-956-171E-2762
2	12.2	42.1	27	6	Sequence 2762, Ap Patent No. 5258283
3	12.2	42.1	69	2	Sequence 30, Appl
4	12.2	42.1	69	2	US-08-410-654B-30
5	12.2	42.1	69	2	US-08-474-851-30
6	12.2	42.1	69	2	US-08-481-560-30
7	11.8	40.7	21	2	US-08-585-593A-13
8	11.6	40.0	36	4	US-08-747-536-10
9	11.6	40.0	36	4	US-08-218-369-7
10	11.6	40.0	36	4	US-08-218-369-15
11	11.6	40.0	36	5	US-09-904-599A-7
12	11.6	40.0	36	5	PCT-US95-03742-7
13	11.6	40.0	61	4	PCT-US95-03742-15
14	11.4	39.3	65	4	US-09-619-213B-45
15	11.2	38.6	25	1	US-09-849-069-37
16	11.2	38.6	25	1	US-08-741-881-28
17	11.2	38.6	25	1	US-08-739-158-28
18	11.2	38.6	25	2	US-08-739-167-28
19	11.2	38.6	25	3	US-08-404-796-28
20	11.2	38.6	25	3	US-08-931-869-28
21	11.2	38.6	25	4	US-09-350-399-28
22	11.2	38.6	33	1	US-09-236-140A-28
23	11.2	38.6	33	1	US-08-741-881-29
24	11.2	38.6	33	2	US-08-739-158-29
25	11.2	38.6	33	3	US-08-739-167-29
26	11.2	38.6	33	3	US-08-404-796-29
27	11.2	38.6	33	4	US-08-931-869-29
28	11.2	38.6	33	4	US-09-350-399-29

33	38.6	11.2	28	4	US-09-236-140A-29	Sequence 29, Appl
36	38.6	11.2	30	2	US-08-642-045B-17	Sequence 17, Appl
36	38.6	11.2	30	2	US-08-852-268-17	Sequence 17, Appl
41	38.6	11.2	31	4	US-09-571-774-2	Sequence 2, Appl
41	38.6	11.2	31	4	US-09-852-385-2	Sequence 2, Appl
47	38.6	11.2	33	4	US-09-422-978-2842	Sequence 2842, Ap
52	38.6	11.2	34	4	US-09-310-463-6	Sequence 6, Appl
52	38.6	11.2	34	4	US-08-842-248A-6	Sequence 6, Appl
70	38.6	11.2	36	3	US-09-364-380-29	Sequence 29, Appl
31	37.9	11	37	1	US-08-323-531-71	Sequence 71, Appl
31	37.9	11	37	1	US-08-198-094-71	Sequence 71, Appl
31	37.9	11	37	1	US-08-480-640A-119	Sequence 119, Appl
31	37.9	11	37	1	US-08-295-802-119	Sequence 119, Appl
31	37.9	11	37	1	US-08-107-794A-71	Sequence 71, Appl
31	37.9	11	37	1	US-08-488-237A-119	Sequence 119, Appl
31	37.9	11	37	1	US-08-375-992A-119	Sequence 119, Appl
31	37.9	11	37	1	US-08-472-679H-119	Sequence 119, Appl
31	37.9	11	37	1	PCT-US93-07424-71	Sequence 71, Appl
31	37.9	11	37	1	PCT-US95-02087-71	Sequence 71, Appl
34	37.9	11	37	1	US-09-581-070-2	Sequence 2, Appl
34	37.9	11	37	1	US-09-581-070-5	Sequence 5, Appl
70	37.9	11	37	2	US-08-488-402A-127	Sequence 127, Appl
70	37.9	11	37	2	US-08-484-552A-127	Sequence 127, Appl
70	37.9	11	37	2	PCT-US96-09472-127	Sequence 127, Appl
19	37.2	10.8	52	1	US-08-365-109B-3	Sequence 1, Appl
19	37.2	10.8	52	1	US-08-365-109B-3	Sequence 1, Appl
20	37.2	10.8	53	3	US-09-560-594-53	Sequence 53, Appl
25	37.2	10.8	55	3	US-08-943-731-336	Sequence 336, Appl
25	37.2	10.8	55	3	US-09-827-998-1097	Sequence 1097, Ap
25	37.2	10.8	57	4	US-09-827-998-1098	Sequence 1098, Ap
25	37.2	10.8	57	4	US-09-827-998-1099	Sequence 1099, Ap
25	37.2	10.8	58	4	US-09-827-998-1100	Sequence 1100, Ap
25	37.2	10.8	59	4	US-09-827-998-1101	Sequence 1101, Ap
25	37.2	10.8	60	4	US-09-827-998-1102	Sequence 1102, Ap
25	37.2	10.8	61	4	US-09-827-998-1103	Sequence 1103, Ap
25	37.2	10.8	62	4	US-09-827-998-1104	Sequence 1104, Ap
27	37.2	10.8	64	3	US-09-253-396A-137	Sequence 137, Appl
29	37.2	10.8	65	4	US-09-304-232-416	Sequence 416, Appl
45	37.2	10.8	66	1	US-08-171-389-130	Sequence 130, Appl
45	37.2	10.8	67	1	US-08-171-389-342	Sequence 342, Appl
45	37.2	10.8	68	1	US-08-123-936-130	Sequence 130, Appl
45	37.2	10.8	68	1	US-08-123-936-342	Sequence 342, Appl
45	37.2	10.8	69	2	US-08-475-228A-130	Sequence 130, Appl
45	37.2	10.8	70	2	US-08-475-228A-342	Sequence 342, Appl
45	37.2	10.8	71	3	US-08-482-080A-130	Sequence 130, Appl
45	37.2	10.8	72	3	US-08-482-080A-342	Sequence 342, Appl
45	37.2	10.8	73	3	US-08-482-080A-342	Sequence 342, Appl
45	37.2	10.8	74	4	US-09-354-947-130	Sequence 130, Appl
45	37.2	10.8	75	4	US-09-354-947-342	Sequence 342, Appl
45	37.2	10.8	76	5	PCT-US93-12388-130	Sequence 130, Appl
45	37.2	10.8	77	5	PCT-US93-12388-342	Sequence 342, Appl
47	37.2	10.8	78	4	US-09-422-978-2286	Sequence 2286, Ap
47	37.2	10.8	79	4	US-09-422-978-3545	Sequence 3545, Ap
48	37.2	10.8	80	1	US-08-119-773-13	Sequence 13, Appl
50	37.2	10.8	81	1	US-08-171-389-343	Sequence 343, Appl
50	37.2	10.8	82	1	US-08-123-936-343	Sequence 343, Appl
50	37.2	10.8	83	2	US-08-633-368-3	Sequence 3, Appl
50	37.2	10.8	83	2	US-08-475-228A-343	Sequence 343, Appl
50	37.2	10.8	84	3	US-08-482-080A-343	Sequence 343, Appl
50	37.2	10.8	85	3	US-09-354-947-343	Sequence 343, Appl
50	37.2	10.8	86	4	PCT-US93-12388-343	Sequence 343, Appl
51	37.2	10.8	87	5	PCT-US93-12388-343	Sequence 39, Appl
51	37.2	10.8	88	1	US-08-220-151-39	Sequence 39, Appl
51	37.2	10.8	89	1	US-08-413-118-39	Sequence 39, Appl
51	37.2	10.8	90	1	US-08-224-657-15	Sequence 16, Appl
51	37.2	10.8	91	1	US-08-257-073-83	Sequence 83, Appl
51	37.2	10.8	92	1	US-08-184-009-16	Sequence 16, Appl
51	37.2	10.8	93	2	US-08-486-969-16	Sequence 16, Appl
51	37.2	10.8	94	2	US-08-417-210A-16	Sequence 16, Appl
51	37.2	10.8	95	2	US-08-458-356-16	Sequence 16, Appl
51	37.2	10.8	96	2	US-08-471-025-16	Sequence 16, Appl
51	37.2	10.8	97	2	US-08-473-445-39	Sequence 39, Appl
51	37.2	10.8	98	3	US-08-460-736-16	Sequence 16, Appl
51	37.2	10.8	99	3	US-09-354-138-16	Sequence 16, Appl
100	37.2	10.8	100	4	US-09-535-370-16	Sequence 16, Appl

C 101	10.8	37.2	51	4	US-09-136-159A-16	Sequence 16, Appl	C 174	10.2	35.2	45	1	US-08-701-269-4	Sequence 4, Appl
C 102	10.8	37.2	51	5	PCT-US96-00547-16	Sequence 16, Appl	C 175	10.2	35.2	45	2	US-08-850-049-86	Sequence 86, Appl
C 103	10.8	37.2	51	6	US-08-956-171E-1736	Sequence 1736, Ap	C 176	10.2	35.2	45	3	US-08-050-478-86	Sequence 86, Appl
C 104	10.6	36.6	29	4	US-09-304-232-644	Sequence 644, App	C 177	10.2	35.2	45	4	US-09-414-117-86	Sequence 86, Appl
C 105	10.6	36.6	30	2	US-09-001-826-11	Sequence 11, Appl	C 178	10.2	35.2	45	5	US-09-678-437-86	Sequence 12, Appl
C 106	10.6	36.6	30	4	US-09-561-825-7	Sequence 7, Appl	C 179	10.2	35.2	46	3	US-09-171-878-12	Sequence 125, App
C 107	10.6	36.6	30	4	US-09-268-884-11	Sequence 11, Appl	C 180	10.2	35.2	46	4	US-09-478-189-125	Sequence 686, App
C 108	10.6	36.6	35	1	US-08-497-312-8	Sequence 8, Appl	C 181	10.2	35.2	47	4	US-09-422-978-686	Sequence 1097, Ap
C 109	10.6	36.6	36	1	US-08-497-312-10	Sequence 10, Appl	C 182	10.2	35.2	47	4	US-09-422-978-1097	Sequence 1171, Ap
C 110	10.6	36.6	38	4	US-09-242-913B-4	Sequence 4, Appl	C 183	10.2	35.2	48	1	US-08-171-389-191	Sequence 191, App
C 111	10.6	36.6	41	4	US-09-666-890-1	Sequence 1, Appl	C 184	10.2	35.2	48	1	US-08-123-936-191	Sequence 191, App
C 112	10.6	36.6	47	4	US-09-422-978-2273	Sequence 2273, Ap	C 185	10.2	35.2	48	3	US-08-475-228A-191	Sequence 191, App
C 113	10.6	36.6	50	2	US-09-282-147-43	Sequence 43, Appl	C 186	10.2	35.2	48	3	US-08-482-080A-191	Sequence 191, App
C 114	10.6	36.6	54	2	US-08-649-981-6	Sequence 6, Appl	C 187	10.2	35.2	48	4	US-09-354-947-191	Sequence 191, App
C 115	10.6	36.6	60	1	US-08-256-964A-7	Sequence 7, Appl	C 188	10.2	35.2	48	5	PCT-US93-12388-191	Sequence 191, App
C 116	10.6	36.6	60	3	US-08-483-511-77	Sequence 77, Appl	C 189	10.2	35.2	50	1	US-08-036-217-19	Sequence 19, Appl
C 117	10.4	35.9	20	4	US-09-422-978-5557	Sequence 5557, Ap	C 190	10.2	35.2	50	1	US-08-105-483-19	Sequence 19, Appl
C 118	10.4	35.9	20	4	US-09-909-595-40	Sequence 40, Appl	C 191	10.2	35.2	50	1	US-08-073-963-35	Sequence 35, Appl
C 119	10.4	35.9	26	1	US-08-599-252-43	Sequence 43, Appl	C 192	10.2	35.2	50	1	US-07-714-687-19	Sequence 19, Appl
C 120	10.4	35.9	26	5	PCT-US96-06352-43	Sequence 43, Appl	C 193	10.2	35.2	50	1	US-08-220-151-42	Sequence 42, Appl
C 121	10.4	35.9	26	5	PCT-US96-06383-43	Sequence 43, Appl	C 194	10.2	35.2	50	1	US-08-220-151-42	Sequence 42, Appl
C 122	10.4	35.9	27	2	US-08-724-354D-19	Sequence 19, Appl	C 195	10.2	35.2	50	1	US-08-171-389-466	Sequence 466, App
C 123	10.4	35.9	27	3	US-09-270-984A-19	Sequence 19, Appl	C 196	10.2	35.2	50	1	US-08-413-118-42	Sequence 42, Appl
C 124	10.4	35.9	29	2	US-08-761-277A-77	Sequence 77, Appl	C 197	10.2	35.2	50	1	US-08-123-936-466	Sequence 466, App
C 125	10.4	35.9	40	4	US-09-731-466-1	Sequence 1, Appl	C 198	10.2	35.2	50	1	US-08-224-391-19	Sequence 19, Appl
C 126	10.4	35.9	41	2	US-08-833-814A-6	Sequence 6, Appl	C 199	10.2	35.2	50	1	US-08-484-304-19	Sequence 19, Appl
C 127	10.4	35.9	47	4	US-09-422-978-133	Sequence 133, App	C 200	10.2	35.2	50	1	US-08-224-657-19	Sequence 19, Appl
C 128	10.4	35.9	47	4	US-09-422-978-430	Sequence 430, App	C 201	10.2	35.2	50	1	US-08-475-063-19	Sequence 19, Appl
C 129	10.4	35.9	47	4	US-09-422-978-734	Sequence 734, App	C 202	10.2	35.2	50	1	US-08-207-793-19	Sequence 19, Appl
C 130	10.4	35.9	47	4	US-09-422-978-2892	Sequence 2892, Ap	C 203	10.2	35.2	50	1	US-08-487-412-35	Sequence 35, Appl
C 131	10.4	35.9	47	4	US-09-422-978-3619	Sequence 3619, Ap	C 204	10.2	35.2	50	1	US-08-709-209-19	Sequence 19, Appl
C 132	10.4	35.9	49	3	US-09-522-494-47	Sequence 47, Appl	C 205	10.2	35.2	50	1	US-08-257-073-86	Sequence 86, Appl
C 133	10.4	35.9	50	4	US-09-428-082B-401	Sequence 401, App	C 206	10.2	35.2	50	1	US-08-303-275-19	Sequence 19, Appl
C 134	10.4	35.9	55	4	US-09-621-976-18457	Sequence 18457, A	C 207	10.2	35.2	50	2	US-08-458-101-19	Sequence 19, Appl
C 135	10.4	35.9	57	4	US-09-428-082B-414	Sequence 414, App	C 208	10.2	35.2	50	2	US-08-486-969-19	Sequence 19, Appl
C 136	10.4	35.9	60	4	US-09-428-082B-415	Sequence 415, App	C 209	10.2	35.2	50	2	US-08-486-969-19	Sequence 19, Appl
C 137	10.4	35.9	61	4	US-09-428-082B-400	Sequence 400, App	C 210	10.2	35.2	50	2	US-08-417-210A-19	Sequence 19, Appl
C 138	10.4	35.9	70	3	US-09-364-380-31	Sequence 31, Appl	C 211	10.2	35.2	50	2	US-08-475-228A-466	Sequence 466, App
C 139	10.4	35.9	71	2	US-08-465-591A-57	Sequence 57, Appl	C 212	10.2	35.2	50	2	US-08-458-356-19	Sequence 19, Appl
C 140	10.4	35.9	71	2	US-08-465-594A-57	Sequence 57, Appl	C 213	10.2	35.2	50	2	US-08-471-025-19	Sequence 19, Appl
C 141	10.4	35.9	71	5	US-08-973-124-242	Sequence 242, App	C 214	10.2	35.2	50	3	US-08-658-665-19	Sequence 19, Appl
C 142	10.4	35.9	71	5	PCT-US96-08014-242	Sequence 242, App	C 215	10.2	35.2	50	3	US-08-482-080A-466	Sequence 466, App
C 143	10.4	35.9	77	6	5182195-3	Patent No. 5182195	C 216	10.2	35.2	50	3	US-08-473-446-42	Sequence 42, Appl
C 144	10.4	35.9	78	6	5182195-6	Patent No. 5182195	C 217	10.2	35.2	50	3	US-08-473-446-42	Sequence 42, Appl
C 145	10.2	35.2	20	3	US-09-407-818-15	Sequence 15, Appl	C 218	10.2	35.2	50	3	US-08-736-19	Sequence 19, Appl
C 146	10.2	35.2	20	4	US-09-853-768-51	Sequence 51, Appl	C 219	10.2	35.2	50	4	US-09-085-273-19	Sequence 19, Appl
C 147	10.2	35.2	21	2	US-08-797-689-20	Sequence 20, Appl	C 220	10.2	35.2	50	4	US-09-354-138-19	Sequence 19, Appl
C 148	10.2	35.2	21	4	US-09-422-978-11708	Sequence 11708, A	C 221	10.2	35.2	50	4	US-09-354-947-466	Sequence 466, App
C 149	10.2	35.2	21	4	US-09-984-186-20	Sequence 20, Appl	C 222	10.2	35.2	50	4	US-09-535-370-19	Sequence 19, Appl
C 150	10.2	35.2	22	2	US-08-474-450A-17	Sequence 17, Appl	C 223	10.2	35.2	50	4	US-09-136-159A-19	Sequence 19, Appl
C 151	10.2	35.2	22	3	US-08-983-466-48	Sequence 48, Appl	C 224	10.2	35.2	50	5	US-09-916-963-19	Sequence 466, App
C 152	10.2	35.2	24	4	US-09-085-686-4	Sequence 4, Appl	C 225	10.2	35.2	50	5	PCT-US93-12388-466	Sequence 466, App
C 153	10.2	35.2	29	2	US-08-716-317-25	Sequence 25, Appl	C 226	10.2	35.2	50	5	PCT-US96-00547-19	Sequence 19, Appl
C 154	10.2	35.2	30	1	US-08-479-487-13	Sequence 13, Appl	C 227	10.2	35.2	56	3	US-09-037-990B-47	Sequence 306, App
C 155	10.2	35.2	30	2	US-08-621-564B-4	Sequence 4, Appl	C 228	10.2	35.2	59	2	US-08-842-842-5	Sequence 5, Appl
C 156	10.2	35.2	30	3	US-08-621-841-51	Sequence 51, Appl	C 229	10.2	35.2	59	2	US-09-052-521C-25	Sequence 25, Appl
C 157	10.2	35.2	30	3	US-09-269-220-4	Sequence 4, Appl	C 230	10.2	35.2	60	3	US-09-126-640-38	Sequence 38, Appl
C 158	10.2	35.2	31	1	US-07-977-284A-233	Sequence 233, App	C 231	10.2	35.2	60	3	US-09-288-292A-38	Sequence 38, Appl
C 159	10.2	35.2	31	1	US-08-256-426B-233	Sequence 233, App	C 232	10.2	35.2	60	3	US-08-956-171B-3478	Sequence 3478, Ap
C 160	10.2	35.2	33	1	US-08-153-848-63	Sequence 63, Appl	C 233	10.2	35.2	64	3	US-08-926-246-38	Sequence 38, Appl
C 161	10.2	35.2	33	1	US-08-372-652-11	Sequence 11, Appl	C 234	10.2	35.2	64	3	US-08-944-495-38	Sequence 38, Appl
C 162	10.2	35.2	33	3	US-09-299-843A-63	Sequence 63, Appl	C 235	10.2	35.2	64	3	US-08-925-588-38	Sequence 38, Appl
C 163	10.2	35.2	33	3	US-09-088-332B-63	Sequence 63, Appl	C 236	10.2	35.2	64	4	US-09-372-044-38	Sequence 38, Appl
C 164	10.2	35.2	33	5	PCT-US93-11153-63	Sequence 63, Appl	C 237	10.2	35.2	65	4	US-08-825-486-38	Sequence 23, Appl
C 165	10.2	35.2	33	5	PCT-US95-16311-11	Sequence 11, Appl	C 238	10.2	35.2	65	4	US-09-052-521C-23	Sequence 23, Appl
C 166	10.2	35.2	34	2	US-08-455-968E-50	Sequence 50, Appl	C 239	10.2	35.2	66	4	US-08-956-171B-2731	Sequence 2731, Ap
C 167	10.2	35.2	35	1	US-08-297-706-4	Sequence 4, Appl	C 240	10.2	35.2	68	3	US-09-275-850-121	Sequence 121, App
C 168	10.2	35.2	35	5	PCT-US93-05759-4	Sequence 4, Appl	C 241	10.2	35.2	70	1	US-08-105-483-449	Sequence 449, App
C 169	10.2	35.2	38	3	US-08-844-274-22	Sequence 22, Appl	C 242	10.2	35.2	70	1	US-08-709-209-449	Sequence 449, App
C 170	10.2	35.2	38	4	US-09-598-421-22	Sequence 22, Appl	C 243	10.2	35.2	70	1	US-08-303-275-161	Sequence 161, App
C 171	10.2	35.2	42	2	US-08-840-887-4	Sequence 4, Appl	C 244	10.2	35.2	70	1	US-08-458-101-449	Sequence 449, App
C 172	10.2	35.2	42	4	US-10-077-480-5	Sequence 5, Appl	C 245	10.2	35.2	70	2	US-08-488-402A-157	Sequence 157, App
C 173	10.2	35.2	45	1	US-08-229-279-4	Sequence 4, Appl	C 246	10.2	35.2	70	2	US-08-484-552A-157	Sequence 157, App

247	10.2	35.2	70	5	PCT-US96-09472-157	Sequence 157, App	320	10	34.5	47	4	US-09-422-978-1676	Sequence 1676, Ap
C 248	10.2	35.2	71	1	US-08-472-255A-108	Sequence 108, App	C 321	10	34.5	47	4	US-09-422-978-2668	Sequence 2668, Ap
C 249	10.2	35.2	71	1	US-08-479-724A-108	Sequence 108, App	C 322	10	34.5	47	4	US-09-422-978-2903	Sequence 2903, Ap
C 250	10.2	35.2	71	3	US-08-472-256B-108	Sequence 108, App	C 323	10	34.5	48	6	5240845-53	Patent No. 5240845
C 251	10.2	35.2	71	3	US-08-472-256B-108	Sequence 108, App	C 324	10	34.5	49	3	US-09-522-494-46	Sequence 46, Appl
C 252	10.2	35.2	71	4	US-08-482-793-108	Sequence 108, App	C 325	10	34.5	50	2	US-08-472-171-27	Sequence 27, Appl
C 253	10.2	35.2	71	4	US-08-482-793-108	Sequence 108, App	C 326	10	34.5	50	2	US-08-472-171-27	Sequence 27, Appl
C 254	10.2	35.2	80	4	PCT-US96-09455A-108	Sequence 108, App	C 327	10	34.5	50	2	US-08-894-526-27	Sequence 27, Appl
C 255	10.2	35.2	80	4	US-09-397-168-47	Sequence 12, Appl	C 328	10	34.5	50	3	US-08-013-047-27	Sequence 27, Appl
C 256	10.2	35.2	80	4	US-09-397-168-47	Sequence 12, Appl	C 329	10	34.5	50	3	US-09-374-597-27	Sequence 27, Appl
C 257	10.2	35.2	16	4	US-09-422-978-6220	Sequence 6220, App	C 330	10	34.5	50	4	US-08-956-171E-2247	Sequence 2247, Ap
C 258	10.2	35.2	19	4	US-08-249-386A-2	Sequence 2, Appl	C 331	10	34.5	50	6	5240845-44	Patent No. 5240845
C 259	10.2	35.2	20	1	US-08-249-386A-10	Sequence 10, Appl	C 332	10	34.5	53	3	US-08-864-473-62	Sequence 62, Appl
C 260	10.2	35.2	20	1	US-08-249-386A-10	Sequence 10, Appl	C 333	10	34.5	53	3	US-09-440-523-62	Sequence 62, Appl
C 261	10.2	35.2	20	3	US-08-227-180B-27	Sequence 27, Appl	C 334	10	34.5	57	2	US-08-663-566A-55	Sequence 55, Appl
C 262	10.2	35.2	20	3	US-09-488-857B-34	Sequence 34, Appl	C 335	10	34.5	57	2	US-08-288-065A-55	Sequence 55, Appl
C 263	10.2	35.2	20	4	US-09-710-200-12	Sequence 12, Appl	C 336	10	34.5	57	2	US-08-362-240A-55	Sequence 55, Appl
C 264	10.2	35.2	20	4	US-09-331-359-6	Sequence 6, Appl	C 337	10	34.5	57	3	US-08-804-372A-17	Sequence 17, Appl
C 265	10.2	35.2	20	4	US-09-331-359-6	Sequence 6, Appl	C 338	10	34.5	57	5	PCT-US95-10245-55	Sequence 55, Appl
C 266	10.2	35.2	20	5	PCT-US95-06160-2	Sequence 2, Appl	C 339	10	34.5	61	4	US-09-549-848B-66	Sequence 66, Appl
C 267	10.2	35.2	20	5	PCT-US95-06160-2	Sequence 2, Appl	C 340	10	34.5	65	4	US-09-495-050A-258	Sequence 258, App
C 268	10.2	35.2	21	4	US-09-337-168-48	Sequence 48, Appl	C 341	10	34.5	75	1	US-07-971-101-6	Sequence 6, Appl
C 269	10.2	35.2	22	4	US-09-337-168-48	Sequence 48, Appl	C 342	9.8	33.8	16	6	5171843-4	Patent No. 5171843
C 270	10.2	35.2	22	4	US-09-337-168-48	Sequence 48, Appl	C 343	9.8	33.8	17	3	US-08-998-099-58	Sequence 58, Appl
C 271	10.2	35.2	24	3	US-09-451-527-131	Sequence 131, App	C 344	9.8	33.8	17	3	US-08-998-099-58	Sequence 58, Appl
C 272	10.2	35.2	24	3	US-09-451-527-131	Sequence 131, App	C 345	9.8	33.8	17	4	US-09-827-998-281	Sequence 281, App
C 273	10.2	35.2	24	3	US-09-522-494-49	Sequence 50, Appl	C 346	9.8	33.8	17	4	US-09-827-998-282	Sequence 282, App
C 274	10.2	35.2	24	3	US-09-522-494-49	Sequence 50, Appl	C 347	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 275	10.2	35.2	24	3	US-09-522-494-51	Sequence 51, Appl	C 348	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 276	10.2	35.2	24	3	US-09-522-494-51	Sequence 51, Appl	C 349	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 277	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 350	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 278	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 351	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 279	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 352	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 280	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 353	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 281	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 354	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 282	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 355	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 283	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 356	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 284	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 357	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 285	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 358	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 286	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 359	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 287	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 360	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 288	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 361	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 289	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 362	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 290	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 363	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 291	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 364	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 292	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 365	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 293	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 366	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 294	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 367	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 295	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 368	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 296	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 369	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 297	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 370	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 298	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 371	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 299	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 372	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 300	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 373	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 301	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 374	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 302	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 375	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 303	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 376	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 304	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 377	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 305	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 378	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 306	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 379	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 307	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 380	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 308	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 381	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 309	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 382	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 310	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 383	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 311	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 384	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 312	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 385	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 313	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 386	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 314	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 387	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 315	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 388	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 316	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 389	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 317	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 390	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 318	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 391	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App
C 319	10.2	35.2	24	3	US-09-522-494-52	Sequence 52, Appl	C 392	9.8	33.8	17	4	US-09-827-998-283	Sequence 283, App

393	9.8	33.8	25	4	US-09-866-108A-15102	Sequence 15102, A	C 466	9.8	33.8	43	3	US-09-150-805-7	Sequence 7, Appli
394	9.8	33.8	25	4	US-09-866-108A-15103	Sequence 15103, A	C 467	9.8	33.8	43	3	US-08-996-069A-5	Sequence 5, Appli
395	9.8	33.8	25	4	US-09-866-108A-15104	Sequence 15104, A	C 468	9.8	33.8	43	3	US-08-996-069A-7	Sequence 7, Appli
396	9.8	33.8	25	4	US-09-866-108A-15105	Sequence 15105, A	C 469	9.8	33.8	43	4	US-09-434-354-4	Sequence 4, Appli
397	9.8	33.8	25	4	US-09-866-108A-15106	Sequence 15106, A	C 470	9.8	33.8	44	1	US-07-832-905B-58	Sequence 58, Appli
398	9.8	33.8	25	4	US-09-866-108A-15107	Sequence 15107, A	C 471	9.8	33.8	44	3	US-08-700-757-58	Sequence 58, Appli
399	9.8	33.8	25	4	US-09-866-108A-15108	Sequence 15108, A	C 472	9.8	33.8	44	3	US-09-100-193-5	Sequence 5, Appli
400	9.8	33.8	25	4	US-09-866-108A-15109	Sequence 15109, A	C 473	9.8	33.8	47	1	US-08-171-389-121	Sequence 121, App
401	9.8	33.8	26	1	US-08-458-023B-9	Sequence 9, Appli	C 474	9.8	33.8	47	1	US-08-123-935-121	Sequence 121, App
402	9.8	33.8	26	1	US-08-445-746-12	Sequence 12, Appli	C 475	9.8	33.8	47	2	US-08-475-228A-121	Sequence 121, App
403	9.8	33.8	26	3	US-09-008-722-12	Sequence 12, Appli	C 476	9.8	33.8	47	2	US-08-700-670A-28	Sequence 28, Appli
404	9.8	33.8	26	4	US-09-197-814-5	Sequence 5, Appli	C 477	9.8	33.8	47	2	US-08-482-080A-121	Sequence 121, App
405	9.8	33.8	26	4	US-09-689-255C-6	Sequence 6, Appli	C 478	9.8	33.8	47	4	US-09-354-947-121	Sequence 121, App
406	9.8	33.8	26	4	US-09-218-446-5	Sequence 5, Appli	C 479	9.8	33.8	47	4	US-09-641-638-1124	Sequence 1124, Ap
407	9.8	33.8	26	4	US-09-920-591-5	Sequence 5, Appli	C 480	9.8	33.8	47	4	US-09-671-317-500	Sequence 500, App
408	9.8	33.8	26	4	US-09-068-357-13	Sequence 13, Appli	C 481	9.8	33.8	47	4	US-09-422-978-56	Sequence 56, App
409	9.8	33.8	27	1	US-08-117-364A-12	Sequence 12, Appli	C 482	9.8	33.8	47	4	US-09-422-978-1012	Sequence 1012, Ap
410	9.8	33.8	27	1	US-08-459-489-5	Sequence 5, Appli	C 483	9.8	33.8	47	4	US-09-422-978-1306	Sequence 1306, Ap
411	9.8	33.8	27	1	US-08-458-686-5	Sequence 5, Appli	C 484	9.8	33.8	47	4	US-09-422-978-2469	Sequence 2469, Ap
412	9.8	33.8	27	1	US-07-843-350C-5	Sequence 5, Appli	C 485	9.8	33.8	47	4	US-09-422-978-2958	Sequence 2958, Ap
413	9.8	33.8	27	2	US-08-457-733-12	Sequence 12, Appli	C 486	9.8	33.8	47	4	US-09-422-978-2979	Sequence 2979, Ap
414	9.8	33.8	27	3	US-08-457-986A-12	Sequence 12, Appli	C 487	9.8	33.8	47	4	US-09-422-978-3012	Sequence 3012, Ap
415	9.8	33.8	27	5	PCT-US93-01559-5	Sequence 5, Appli	C 488	9.8	33.8	47	4	US-09-422-978-3201	Sequence 3201, Ap
416	9.8	33.8	28	2	US-08-859-998-1098	Sequence 1098, Ap	C 489	9.8	33.8	47	4	US-09-422-978-3368	Sequence 3368, Ap
417	9.8	33.8	28	2	US-08-859-998-1114	Sequence 1114, Ap	C 490	9.8	33.8	47	4	US-09-422-978-3630	Sequence 3630, Ap
418	9.8	33.8	28	3	US-08-828-533-29	Sequence 29, Appli	C 491	9.8	33.8	47	5	PCT-US93-12388-121	Sequence 121, App
419	9.8	33.8	28	4	US-09-225-928-1114	Sequence 1114, Ap	C 492	9.8	33.8	50	3	US-08-833-167-84	Sequence 84, Appli
420	9.8	33.8	28	4	US-09-225-928-1114	Sequence 1114, Ap	C 493	9.8	33.8	50	3	US-09-390-867A-31	Sequence 31, Appli
421	9.8	33.8	28	4	US-09-225-928-1114	Sequence 1098, Ap	C 494	9.8	33.8	50	4	US-09-548-260-31	Sequence 31, Appli
422	9.8	33.8	28	4	US-09-225-201B-1114	Sequence 1114, Ap	C 495	9.8	33.8	50	4	US-09-344-837A-84	Sequence 84, Appli
423	9.8	33.8	28	4	US-09-772-156-29	Sequence 29, Appli	C 496	9.8	33.8	50	4	US-09-554-929-182	Sequence 182, App
424	9.8	33.8	29	1	US-08-445-746-10	Sequence 10, Appli	C 497	9.8	33.8	54	3	US-08-369-822C-30	Sequence 30, Appli
425	9.8	33.8	29	3	US-09-008-722-10	Sequence 10, Appli	C 498	9.8	33.8	54	3	US-08-582-776C-45	Sequence 45, Appli
426	9.8	33.8	30	1	US-07-940-605A-13	Sequence 13, Appli	C 499	9.8	33.8	54	3	US-08-434-831B-42	Sequence 42, Appli
427	9.8	33.8	30	1	US-08-182-530-4	Sequence 4, Appli	C 500	9.8	33.8	55	3	US-08-434-831A-17	Sequence 17, Appli
428	9.8	33.8	30	1	US-08-050-058B-4	Sequence 4, Appli	C 501	9.8	33.8	55	4	US-09-509-748-4	Sequence 4, Appli
429	9.8	33.8	30	1	US-08-463-587A-4	Sequence 4, Appli	C 502	9.8	33.8	60	1	US-08-464-531-18	Sequence 18, Appli
430	9.8	33.8	30	2	US-08-463-667A-7	Sequence 7, Appli	C 503	9.8	33.8	60	2	US-08-461-598-18	Sequence 18, Appli
431	9.8	33.8	30	2	US-08-441-871-8	Sequence 8, Appli	C 504	9.8	33.8	60	3	US-08-322-137-18	Sequence 18, Appli
432	9.8	33.8	30	2	US-08-418-085-21	Sequence 21, Appli	C 505	9.8	33.8	60	3	US-08-582-333A-9	Sequence 9, Appli
433	9.8	33.8	30	2	US-08-690-096-13	Sequence 13, Appli	C 506	9.8	33.8	61	4	US-09-313-221A-80	Sequence 80, Appli
434	9.8	33.8	30	2	US-08-923-854-4	Sequence 4, Appli	C 507	9.8	33.8	62	2	US-08-210-763B-5	Sequence 5, Appli
435	9.8	33.8	30	3	US-09-099-011A-21	Sequence 21, Appli	C 508	9.8	33.8	62	4	US-09-106-075A-5	Sequence 5, Appli
436	9.8	33.8	30	3	US-09-490-825-2	Sequence 2, Appli	C 509	9.8	33.8	63	2	US-09-159-385-7	Sequence 7, Appli
437	9.8	33.8	30	4	US-09-898-627-2	Sequence 2, Appli	C 510	9.8	33.8	63	3	US-09-186-277-7	Sequence 7, Appli
438	9.8	33.8	30	4	US-09-397-955C-16	Sequence 16, Appli	C 511	9.8	33.8	64	1	US-08-471-364A-2	Sequence 2, Appli
439	9.8	33.8	30	4	US-09-098-877B-21	Sequence 21, Appli	C 512	9.8	33.8	67	3	US-08-483-511-55	Sequence 55, Appli
440	9.8	33.8	30	4	US-09-381-393A-7	Sequence 7, Appli	C 513	9.8	33.8	67	5	PCT-US93-01009-55	Sequence 55, Appli
441	9.8	33.8	30	5	PCT-US91-09133-4	Sequence 4, Appli	C 514	9.8	33.8	68	2	US-09-121-527-3	Sequence 3, Appli
442	9.8	33.8	31	4	US-09-206-898-22	Sequence 22, Appli	C 515	9.8	33.8	70	1	US-08-434-001-179	Sequence 179, App
443	9.8	33.8	31	4	US-08-201-118-15	Sequence 15, Appli	C 516	9.8	33.8	70	1	US-08-433-585-179	Sequence 179, App
444	9.8	33.8	31	4	US-08-201-118-15	Sequence 21, Appli	C 517	9.8	33.8	70	1	US-08-434-425-179	Sequence 179, App
445	9.8	33.8	31	2	US-08-238-821B-15	Sequence 15, Appli	C 518	9.8	33.8	70	3	US-08-437-667-179	Sequence 179, App
446	9.8	33.8	31	2	US-08-238-821B-15	Sequence 21, Appli	C 519	9.8	33.8	70	3	US-08-906-955-179	Sequence 179, App
447	9.8	33.8	31	2	US-08-238-821B-21	Sequence 21, Appli	C 520	9.8	33.8	70	3	US-08-945-909-179	Sequence 179, App
448	9.8	33.8	31	2	US-09-855-341-13	Sequence 13, Appli	C 521	9.8	33.8	70	4	US-09-396-002A-179	Sequence 179, App
449	9.8	33.8	31	5	PCT-US95-05744-15	Sequence 15, Appli	C 522	9.8	33.8	70	4	US-10-077-319-179	Sequence 179, App
450	9.8	33.8	31	5	PCT-US95-05744-21	Sequence 21, Appli	C 523	9.8	33.8	70	5	PCT-US96-06060-179	Sequence 179, App
451	9.8	33.8	34	1	US-07-982-174-4	Sequence 4, Appli	C 524	9.8	33.8	71	2	US-08-482-182-45	Sequence 42, Appli
452	9.8	33.8	34	1	US-08-589-528-4	Sequence 4, Appli	C 525	9.8	33.8	71	2	US-08-482-182-45	Sequence 45, Appli
453	9.8	33.8	34	2	US-08-392-625-7	Sequence 7, Appli	C 526	9.8	33.8	77	4	US-09-621-976-8652	Sequence 8652, Ap
454	9.8	33.8	34	2	US-08-466-961A-7	Sequence 7, Appli	C 527	9.8	33.8	77	4	US-08-290-592B-40	Sequence 40, Appli
455	9.8	33.8	34	3	US-07-901-713A-19	Sequence 19, Appli	C 528	9.8	33.8	78	1	US-08-817-335-2	Sequence 2, Appli
456	9.8	33.8	34	5	PCT-US93-11492-4	Sequence 4, Appli	C 529	9.8	33.8	78	4	US-09-397-680A-1	Sequence 1, Appli
457	9.8	33.8	35	4	US-09-381-393A-3	Sequence 3, Appli	C 530	9.8	33.8	78	4	US-09-949-404-1	Sequence 1, Appli
458	9.8	33.8	36	4	US-09-198-115C-19	Sequence 19, Appli	C 531	9.8	33.8	78	5	PCT-US96-09448-40	Sequence 40, Appli
459	9.8	33.8	37	1	US-08-464-531-4	Sequence 4, Appli	C 532	9.8	33.8	80	1	US-07-832-905B-61	Sequence 61, Appli
460	9.8	33.8	37	1	US-08-461-598-4	Sequence 4, Appli	C 533	9.8	33.8	80	1	US-07-832-905B-62	Sequence 62, Appli
461	9.8	33.8	37	3	US-08-322-137-4	Sequence 4, Appli	C 534	9.8	33.8	80	2	US-08-700-757-61	Sequence 61, Appli
462	9.8	33.8	40	3	US-08-833-167-85	Sequence 85, Appli	C 535	9.8	33.8	80	2	US-08-700-757-61	Sequence 61, Appli
463	9.8	33.8	40	3	US-09-344-837A-85	Sequence 85, Appli	C 536	9.8	33.1	22	4	US-09-026-033-5	Sequence 5, Appli
464	9.8	33.8	42	3	US-08-434-099A-16	Sequence 16, Appli	C 537	9.8	33.1	24	2	US-08-451-822A-11	Sequence 11, Appli
465	9.8	33.8	43	3	US-09-150-805-5	Sequence 5, Appli	C 538	9.8	33.1	24	4	US-08-323-430-11	Sequence 11, Appli

539	9.6	33.1	24	4	US-09-486-382B-17	Sequence 17, Appl	612	9.6	33.1	36	3	US-08-767-942A-35	Sequence 35, Appl
540	9.6	33.1	24	4	US-09-812-028-1	Sequence 1, Appl	C 613	9.6	33.1	36	3	US-09-440-001-1	Sequence 1, Appl
541	9.6	33.1	26	2	US-08-639-857-9	Sequence 9, Appl	C 614	9.6	33.1	36	3	US-09-440-001-3	Sequence 3, Appl
542	9.6	33.1	26	5	PCT-US93-08094-33	Sequence 33, Appl	615	9.6	33.1	36	4	US-09-518-914-26	Sequence 26, Appl
543	9.6	33.1	27	3	US-09-101-683-5	Sequence 5, Appl	C 616	9.6	33.1	36	4	US-09-605-685-1	Sequence 1, Appl
544	9.6	33.1	27	3	US-08-106-182-17	Sequence 17, Appl	C 617	9.6	33.1	36	4	US-09-605-685-3	Sequence 3, Appl
545	9.6	33.1	27	3	US-08-106-182-23	Sequence 23, Appl	618	9.6	33.1	36	4	US-09-506-859-8	Sequence 8, Appl
546	9.6	33.1	27	4	US-09-227-357-4	Sequence 4, Appl	619	9.6	33.1	36	5	PCT-US95-15428-8	Sequence 8, Appl
547	9.6	33.1	27	4	US-09-280-839-7	Sequence 7, Appl	620	9.6	33.1	37	1	US-08-049-264C-55	Sequence 55, Appl
548	9.6	33.1	27	4	US-09-411-977-19	Sequence 19, Appl	621	9.6	33.1	37	1	US-08-476-562-55	Sequence 55, Appl
549	9.6	33.1	27	4	US-09-479-729B-24	Sequence 24, Appl	622	9.6	33.1	37	1	US-08-479-723A-55	Sequence 55, Appl
550	9.6	33.1	27	4	US-09-257-179-4	Sequence 4, Appl	623	9.6	33.1	37	5	PCT-US94-04310-55	Sequence 55, Appl
551	9.6	33.1	27	4	US-09-149-476-4	Sequence 4, Appl	624	9.6	33.1	39	3	US-08-564-496C-7	Sequence 7, Appl
552	9.6	33.1	27	4	US-08-288-143-4	Sequence 4, Appl	625	9.6	33.1	39	4	US-09-506-859-7	Sequence 7, Appl
553	9.6	33.1	27	4	US-09-487-792-26	Sequence 26, Appl	626	9.6	33.1	39	4	US-09-596-248D-26	Sequence 26, Appl
554	9.6	33.1	27	4	US-09-152-060-4	Sequence 4, Appl	627	9.6	33.1	39	5	PCT-US95-15428-7	Sequence 7, Appl
555	9.6	33.1	27	4	US-09-908-594-26	Sequence 26, Appl	628	9.6	33.1	40	2	US-08-821-022A-4	Sequence 4, Appl
556	9.6	33.1	27	4	US-09-461-325-4	Sequence 4, Appl	629	9.6	33.1	41	1	US-08-468-220-28	Sequence 28, Appl
557	9.6	33.1	27	4	US-09-489-847-4	Sequence 4, Appl	630	9.6	33.1	41	2	US-08-468-698-28	Sequence 28, Appl
558	9.6	33.1	27	4	US-09-231-788-19	Sequence 19, Appl	631	9.6	33.1	41	3	US-08-194-664A-28	Sequence 28, Appl
559	9.6	33.1	27	4	US-09-512-363-20	Sequence 20, Appl	632	9.6	33.1	41	4	US-09-565-156A-2	Sequence 2, Appl
560	9.6	33.1	27	4	US-09-512-363-20	Sequence 20, Appl	C 633	9.6	33.1	41	4	US-09-232-273-5	Sequence 5, Appl
561	9.6	33.1	27	4	US-09-512-363-26	Sequence 26, Appl	634	9.6	33.1	41	5	PCT-US94-0153A-28	Sequence 28, Appl
562	9.6	33.1	27	4	US-09-176-200-20	Sequence 20, Appl	635	9.6	33.1	41	5	PCT-US95-10426-28	Sequence 28, Appl
563	9.6	33.1	27	4	US-09-176-200-26	Sequence 26, Appl	636	9.6	33.1	42	2	US-08-732-612-5	Sequence 5, Appl
564	9.6	33.1	27	4	US-09-205-258-4	Sequence 4, Appl	637	9.6	33.1	42	3	US-09-306-998-16	Sequence 16, Appl
565	9.6	33.1	27	4	US-09-630-454-4	Sequence 4, Appl	C 638	9.6	33.1	44	1	US-08-049-264C-54	Sequence 54, Appl
566	9.6	33.1	27	4	US-09-482-271-12	Sequence 12, Appl	C 639	9.6	33.1	44	1	US-08-476-562-54	Sequence 54, Appl
567	9.6	33.1	27	4	US-09-482-271-18	Sequence 18, Appl	C 640	9.6	33.1	44	1	US-08-479-723A-54	Sequence 54, Appl
568	9.6	33.1	27	4	US-09-482-273-4	Sequence 4, Appl	641	9.6	33.1	44	4	US-09-301-593-73	Sequence 73, Appl
569	9.6	33.1	27	4	US-09-904-615-4	Sequence 4, Appl	C 642	9.6	33.1	44	5	PCT-US94-04310-54	Sequence 54, Appl
570	9.6	33.1	27	4	US-09-369-347-4	Sequence 4, Appl	C 643	9.6	33.1	45	3	US-09-091-814-105	Sequence 105, Appl
571	9.6	33.1	27	4	US-09-148-545-4	Sequence 4, Appl	644	9.6	33.1	45	3	US-09-091-814-107	Sequence 107, Appl
572	9.6	33.1	27	4	US-09-584-829-27	Sequence 27, Appl	C 645	9.6	33.1	46	1	US-08-298-073-20	Sequence 20, Appl
573	9.6	33.1	27	4	US-09-572-406B-22	Sequence 22, Appl	C 646	9.6	33.1	46	1	US-08-794-133-20	Sequence 20, Appl
574	9.6	33.1	27	4	US-09-800-729-4	Sequence 4, Appl	647	9.6	33.1	46	3	US-09-065-104-10	Sequence 10, Appl
575	9.6	33.1	27	4	US-09-557-170A-15	Sequence 15, Appl	C 648	9.6	33.1	46	3	US-09-115-566-20	Sequence 20, Appl
576	9.6	33.1	27	4	US-09-557-170A-21	Sequence 21, Appl	C 649	9.6	33.1	47	1	US-08-171-389-221	Sequence 221, Appl
577	9.6	33.1	27	4	US-09-369-248A-7	Sequence 7, Appl	C 650	9.6	33.1	47	1	US-08-123-936-221	Sequence 221, Appl
578	9.6	33.1	27	4	US-10-012-542-4	Sequence 4, Appl	C 651	9.6	33.1	47	2	US-08-475-228A-221	Sequence 221, Appl
579	9.6	33.1	27	4	US-08-716-129-4	Sequence 4, Appl	C 652	9.6	33.1	47	3	US-08-482-080A-221	Sequence 221, Appl
580	9.6	33.1	27	4	US-10-153-064-28	Sequence 28, Appl	653	9.6	33.1	47	3	US-08-944-368A-28	Sequence 28, Appl
581	9.6	33.1	28	3	US-08-348-548-88	Sequence 88, Appl	654	9.6	33.1	47	4	US-09-820-764-28	Sequence 28, Appl
582	9.6	33.1	28	4	US-09-614-748A-19	Sequence 19, Appl	C 655	9.6	33.1	47	4	US-09-354-947-221	Sequence 221, Appl
583	9.6	33.1	28	5	PCT-US95-15716-88	Sequence 88, Appl	656	9.6	33.1	47	4	US-09-641-638-1059	Sequence 1059, Appl
584	9.6	33.1	29	3	US-08-844-274-7	Sequence 7, Appl	C 657	9.6	33.1	47	4	US-09-641-638-1251	Sequence 1251, Appl
585	9.6	33.1	29	4	US-09-598-421-7	Sequence 7, Appl	658	9.6	33.1	47	4	US-09-671-317-876	Sequence 876, Appl
586	9.6	33.1	29	4	US-08-324-243-30	Sequence 30, Appl	C 659	9.6	33.1	47	4	US-09-422-978-1088	Sequence 1088, Appl
587	9.6	33.1	30	1	US-08-532-390-30	Sequence 30, Appl	C 660	9.6	33.1	47	4	US-09-422-978-3323	Sequence 3323, Appl
588	9.6	33.1	30	3	US-08-717-294-30	Sequence 30, Appl	661	9.6	33.1	47	4	US-09-422-978-3850	Sequence 3850, Appl
589	9.6	33.1	30	4	US-09-561-825-6	Sequence 6, Appl	662	9.6	33.1	47	4	US-09-837-644-1	Sequence 1, Appl
590	9.6	33.1	30	5	PCT-US95-11511-30	Sequence 30, Appl	663	9.6	33.1	47	4	US-09-986-118A-28	Sequence 28, Appl
591	9.6	33.1	31	4	US-09-593-012-97	Sequence 97, Appl	664	9.6	33.1	47	4	PCT-US93-12388-221	Sequence 221, Appl
592	9.6	33.1	31	4	US-08-246-704-1	Sequence 1, Appl	C 665	9.6	33.1	49	4	US-08-897-956A-31	Sequence 31, Appl
593	9.6	33.1	32	2	US-08-467-202-3	Sequence 3, Appl	666	9.6	33.1	50	1	US-08-171-389-341	Sequence 341, Appl
594	9.6	33.1	32	4	US-09-270-140A-12	Sequence 12, Appl	667	9.6	33.1	50	1	US-08-171-389-593	Sequence 593, Appl
595	9.6	33.1	32	6	5514565-1	Patent No. 5514565	668	9.6	33.1	50	1	US-08-123-936-341	Sequence 341, Appl
596	9.6	33.1	33	1	US-08-094-534-20	Sequence 20, Appl	669	9.6	33.1	50	1	US-08-123-936-593	Sequence 593, Appl
597	9.6	33.1	33	1	US-08-532-390-38	Sequence 38, Appl	670	9.6	33.1	50	1	US-08-123-936-593	Sequence 593, Appl
598	9.6	33.1	33	2	US-08-581-543-20	Sequence 20, Appl	671	9.6	33.1	50	2	US-08-475-228A-341	Sequence 341, Appl
599	9.6	33.1	33	3	US-08-717-294-38	Sequence 38, Appl	672	9.6	33.1	50	2	US-08-475-228A-593	Sequence 593, Appl
600	9.6	33.1	33	4	US-09-404-652B-3	Sequence 3, Appl	673	9.6	33.1	50	3	US-08-482-080A-341	Sequence 341, Appl
601	9.6	33.1	33	4	US-09-276-654C-3	Sequence 3, Appl	674	9.6	33.1	50	3	US-08-482-080A-593	Sequence 593, Appl
602	9.6	33.1	33	5	PCT-US94-08000-20	Sequence 20, Appl	675	9.6	33.1	50	4	US-09-354-947-341	Sequence 341, Appl
603	9.6	33.1	34	3	US-09-040-025-15	Sequence 15, Appl	676	9.6	33.1	50	4	US-09-354-947-593	Sequence 593, Appl
604	9.6	33.1	34	3	US-09-040-025-15	Sequence 15, Appl	C 677	9.6	33.1	50	4	US-08-585-593A-4	Sequence 4, Appl
605	9.6	33.1	35	1	US-07-744-282C-105	Sequence 105, Appl	678	9.6	33.1	50	5	PCT-US93-12388-341	Sequence 341, Appl
606	9.6	33.1	35	1	US-08-558-735-22	Sequence 22, Appl	679	9.6	33.1	50	5	PCT-US93-12388-593	Sequence 593, Appl
607	9.6	33.1	35	3	US-08-906-480-22	Sequence 22, Appl	C 680	9.6	33.1	53	2	US-08-485-969-46	Sequence 46, Appl
608	9.6	33.1	35	3	US-09-113-750A-43	Sequence 43, Appl	C 681	9.6	33.1	54	2	US-08-485-969-46	Sequence 46, Appl
609	9.6	33.1	35	4	US-09-774-377-22	Sequence 22, Appl	C 682	9.6	33.1	54	2	US-08-649-981-129	Sequence 129, Appl
610	9.6	33.1	35	5	PCT-US92-06821A-51	Sequence 51, Appl	683	9.6	33.1	60	3	US-08-478-097A-32	Sequence 32, Appl
611	9.6	33.1	36	3	US-08-564-496C-8	Sequence 8, Appl	684	9.6	33.1	60	4	US-09-179-556-57	Sequence 57, Appl

831	9.4	32.4	39	4	US-09-622-540A-17	Sequence 17, Appl	C 904	9.4	32.4	61	4	US-08-638-524B-21	Sequence 21, Appl
832	9.4	32.4	39	4	US-09-622-540A-17	Sequence 17, Appl	905	9.4	32.4	62	4	US-09-502-558-20	Sequence 20, Appl
C 833	9.4	32.4	39	4	US-09-350-982C-10	Sequence 10, Appl	906	9.4	32.4	62	4	US-08-956-171E-1684	Sequence 1684, Ap
C 834	9.4	32.4	40	2	US-08-628-422-48	Sequence 48, Appl	907	9.4	32.4	63	2	US-08-350-260A-201	Sequence 201, Appl
C 835	9.4	32.4	40	4	US-09-233-139-7	Sequence 7, Appl	908	9.4	32.4	63	4	US-09-104-337A-201	Sequence 201, Appl
C 836	9.4	32.4	40	4	US-08-436-082B-418	Sequence 118, App	C 909	9.4	32.4	64	4	US-09-586-546-40	Sequence 40, Appl
C 837	9.4	32.4	41	3	US-08-813-507-152	Sequence 152, App	C 910	9.4	32.4	64	4	US-09-065-914B-4	Sequence 4, Appl
C 838	9.4	32.4	41	4	US-08-464-453-152	Sequence 152, App	911	9.4	32.4	71	2	US-08-894-578-130	Sequence 190, Appl
C 839	9.4	32.4	41	4	US-09-350-982C-8	Sequence 8, Appl	912	9.4	32.4	71	4	US-09-364-902-43	Sequence 43, Appl
C 840	9.4	32.4	41	4	US-09-442-021-23	Sequence 23, Appl	913	9.4	32.4	71	4	US-09-363-939A-28	Sequence 28, Appl
C 841	9.4	32.4	42	3	US-09-237-712-39	Sequence 39, Appl	914	9.4	32.4	71	4	US-08-854-662-43	Sequence 43, Appl
C 842	9.4	32.4	43	3	US-09-237-712-39	Sequence 30, Appl	C 915	9.4	32.4	72	3	US-08-821-827C-28	Sequence 28, Appl
C 843	9.4	32.4	45	3	US-09-312-285-6	Sequence 6, Appl	C 916	9.4	32.4	72	4	US-09-290-202B-28	Sequence 28, Appl
C 844	9.4	32.4	45	3	US-08-312-285-7	Sequence 7, Appl	917	9.4	32.4	72	4	US-09-313-294A-4205	Sequence 4205, Ap
C 845	9.4	32.4	45	3	US-08-312-286-6	Sequence 6, Appl	918	9.4	32.4	78	4	US-09-621-976-12398	Sequence 12398, A
C 846	9.4	32.4	45	3	US-08-312-286-7	Sequence 7, Appl	C 919	9.4	32.4	79	5	PCT-US95-12401A-56	Sequence 56, Appl
C 847	9.4	32.4	45	3	US-08-312-288-6	Sequence 6, Appl	C 920	9.4	32.4	79	5	PCT-US95-12401A-56	Sequence 56, Appl
C 848	9.4	32.4	45	3	US-08-312-288-7	Sequence 7, Appl	C 921	9.4	32.4	80	1	US-08-471-985A-53	Sequence 53, Appl
C 849	9.4	32.4	45	3	US-08-728-764-6	Sequence 6, Appl	C 922	9.4	32.4	80	1	US-08-471-985A-71	Sequence 71, Appl
C 850	9.4	32.4	45	4	US-08-728-764-7	Sequence 7, Appl	C 923	9.4	32.4	80	1	US-08-471-985A-78	Sequence 78, Appl
C 851	9.4	32.4	45	4	US-08-312-304B-4	Sequence 4, Appl	C 924	9.4	32.4	80	1	US-08-472-255A-157	Sequence 157, App
C 852	9.4	32.4	45	4	US-08-312-304B-5	Sequence 5, Appl	C 925	9.4	32.4	80	1	US-08-472-256B-157	Sequence 157, App
C 853	9.4	32.4	45	4	US-09-728-792-6	Sequence 6, Appl	C 926	9.4	32.4	80	3	US-08-472-256B-157	Sequence 157, App
C 854	9.4	32.4	45	4	US-09-728-792-7	Sequence 7, Appl	C 927	9.4	32.4	80	3	US-08-952-793-157	Sequence 157, App
C 855	9.4	32.4	45	4	US-08-850-964-6	Sequence 6, Appl	C 928	9.4	32.4	80	3	US-08-952-793-157	Sequence 157, App
C 856	9.4	32.4	45	4	US-08-850-964-7	Sequence 7, Appl	C 929	9.4	32.4	80	4	US-09-849-928-157	Sequence 157, App
C 857	9.4	32.4	47	4	US-08-641-638-1106	Sequence 1106, Ap	C 930	9.4	32.4	80	4	US-09-849-928-157	Sequence 157, App
C 858	9.4	32.4	47	4	US-08-422-978-952	Sequence 952, App	C 931	9.4	32.4	80	5	PCT-US95-12401A-53	Sequence 53, Appl
C 859	9.4	32.4	47	4	US-08-422-978-952	Sequence 1054, Ap	C 932	9.4	32.4	80	5	PCT-US95-12401A-71	Sequence 71, Appl
C 860	9.4	32.4	47	4	US-08-422-978-1681	Sequence 1681, Ap	C 933	9.4	32.4	80	5	PCT-US95-12401A-78	Sequence 78, Appl
C 861	9.4	32.4	47	4	US-08-422-978-1965	Sequence 1965, Ap	C 934	9.4	32.4	80	5	PCT-US96-09455A-157	Sequence 157, App
C 862	9.4	32.4	47	4	US-08-422-978-2218	Sequence 2218, Ap	C 935	9.4	32.4	80	5	PCT-US96-09455A-172	Sequence 172, App
C 863	9.4	32.4	47	4	US-08-422-978-2337	Sequence 2337, Ap	C 936	9.2	31.7	17	4	US-09-827-998-846	Sequence 846, App
C 864	9.4	32.4	47	4	US-08-422-978-3699	Sequence 3699, Ap	C 937	9.2	31.7	18	1	US-08-599-253-22	Sequence 22, Appl
C 865	9.4	32.4	47	4	US-08-422-978-3710	Sequence 3710, Ap	C 938	9.2	31.7	18	1	US-08-436-074-22	Sequence 22, Appl
C 866	9.4	32.4	48	4	US-08-586-546-43	Sequence 43, Appl	C 939	9.2	31.7	18	5	PCT-US96-06352-22	Sequence 22, Appl
C 867	9.4	32.4	48	4	US-08-065-914B-2	Sequence 2, Appl	C 940	9.2	31.7	18	5	PCT-US96-06352-22	Sequence 22, Appl
C 868	9.4	32.4	48	4	US-08-623-326-37	Sequence 37, Appl	C 941	9.2	31.7	19	1	US-08-379-081B-130	Sequence 130, Appl
C 869	9.4	32.4	49	3	US-09-109-063-28	Sequence 28, Appl	C 942	9.2	31.7	19	1	US-08-379-081B-146	Sequence 146, Appl
C 870	9.4	32.4	49	3	US-09-109-063-29	Sequence 29, Appl	C 943	9.2	31.7	19	1	US-08-379-078-130	Sequence 130, Appl
C 871	9.4	32.4	49	3	US-08-874-825-46	Sequence 46, Appl	C 944	9.2	31.7	19	1	US-08-379-078-130	Sequence 130, Appl
C 872	9.4	32.4	49	3	US-08-874-825-46	Sequence 46, Appl	C 945	9.2	31.7	19	3	US-08-651-999A-8	Sequence 8, Appl
C 873	9.4	32.4	49	3	US-08-663-824-46	Sequence 46, Appl	C 946	9.2	31.7	19	3	US-08-532-896-53	Sequence 53, Appl
C 874	9.4	32.4	49	4	US-08-231-303-46	Sequence 231, Appl	C 947	9.2	31.7	19	3	US-08-561-810-84	Sequence 84, Appl
C 875	9.4	32.4	49	4	US-09-448-310-28	Sequence 28, Appl	C 948	9.2	31.7	19	3	US-08-352-902D-84	Sequence 84, Appl
C 876	9.4	32.4	50	3	US-09-237-712-80	Sequence 80, Appl	C 949	9.2	31.7	19	3	US-09-385-752-8	Sequence 8, Appl
C 877	9.4	32.4	50	4	US-09-554-929-12	Sequence 12, Appl	C 950	9.2	31.7	19	4	US-09-343-681C-85	Sequence 85, Appl
C 878	9.4	32.4	50	4	US-08-956-171E-2665	Sequence 2665, Ap	C 951	9.2	31.7	19	4	US-09-375-318-29	Sequence 29, Appl
C 879	9.4	32.4	51	4	US-08-956-171E-2477	Sequence 2477, Ap	C 952	9.2	31.7	19	4	US-09-375-318-43	Sequence 43, Appl
C 880	9.4	32.4	51	4	US-08-621-976-3693	Sequence 621, Appl	C 953	9.2	31.7	19	4	US-09-265-503B-84	Sequence 84, Appl
C 881	9.4	32.4	51	4	US-08-443-199C-737	Sequence 737, App	C 954	9.2	31.7	20	1	US-08-190-711-4	Sequence 4, Appl
C 882	9.4	32.4	52	4	US-08-956-171E-2653	Sequence 2653, Ap	C 955	9.2	31.7	20	1	US-08-455-896-12	Sequence 12, Appl
C 883	9.4	32.4	54	1	US-07-744-282C-91	Sequence 91, Appl	C 956	9.2	31.7	20	2	US-08-249-386A-1	Sequence 1, Appl
C 884	9.4	32.4	54	1	US-08-956-171E-1892	Sequence 1892, Ap	C 957	9.2	31.7	20	2	US-08-933-149-12	Sequence 12, Appl
C 885	9.4	32.4	54	5	PCT-US92-06821A-74	Sequence 74, Appl	C 958	9.2	31.7	20	3	US-09-082-343-12	Sequence 12, Appl
C 886	9.4	32.4	56	1	US-08-102-474-10	Sequence 10, Appl	C 959	9.2	31.7	20	3	US-09-082-253-12	Sequence 12, Appl
C 887	9.4	32.4	56	1	US-08-414-019A-10	Sequence 10, Appl	C 960	9.2	31.7	20	3	US-08-487-799-66	Sequence 66, Appl
C 888	9.4	32.4	56	2	US-08-976-413A-259	Sequence 259, App	C 961	9.2	31.7	20	3	US-08-777-266A-9	Sequence 9, Appl
C 889	9.4	32.4	57	2	US-08-465-591A-19	Sequence 19, Appl	C 962	9.2	31.7	20	3	US-09-287-796-88	Sequence 88, Appl
C 890	9.4	32.4	57	2	US-08-465-591A-19	Sequence 19, Appl	C 963	9.2	31.7	20	3	US-09-287-796-88	Sequence 88, Appl
C 891	9.4	32.4	57	3	US-08-973-124-204	Sequence 204, Appl	C 964	9.2	31.7	20	3	US-09-130-616-88	Sequence 88, Appl
C 892	9.4	32.4	57	5	PCT-US96-08014-204	Sequence 204, App	C 965	9.2	31.7	20	3	US-09-130-616-89	Sequence 89, Appl
C 893	9.4	32.4	58	4	US-09-621-976-12180	Sequence 12180, A	C 966	9.2	31.7	20	3	US-09-560-594-49	Sequence 49, Appl
C 894	9.4	32.4	59	4	US-08-775-319-10	Sequence 10, Appl	C 967	9.2	31.7	20	3	US-09-180-437-38	Sequence 38, Appl
C 895	9.4	32.4	59	4	US-09-532-419A-10	Sequence 10, Appl	C 968	9.2	31.7	20	4	US-09-378-718-5	Sequence 5, Appl
C 896	9.4	32.4	60	3	US-08-237-712-66	Sequence 66, Appl	C 969	9.2	31.7	20	4	US-09-488-856A-29	Sequence 29, Appl
C 897	9.4	32.4	61	3	US-08-593-455B-21	Sequence 21, Appl	C 970	9.2	31.7	20	4	US-09-326-186B-9	Sequence 9, Appl
C 898	9.4	32.4	61	3	US-09-069-781B-21	Sequence 21, Appl	C 971	9.2	31.7	20	4	US-09-468-872-68	Sequence 68, Appl
C 899	9.4	32.4	61	4	US-08-137-132-21	Sequence 21, Appl	C 972	9.2	31.7	20	4	US-09-354-151-16	Sequence 16, Appl
C 900	9.4	32.4	61	4	US-08-864-564A-21	Sequence 21, Appl	C 973	9.2	31.7	20	4	US-09-527-030G-328	Sequence 328, App
C 901	9.4	32.4	61	4	US-08-094-410-21	Sequence 21, Appl	C 974	9.2	31.7	20	4	US-09-527-030G-334	Sequence 334, App
C 902	9.4	32.4	61	4	US-08-708-123D-21	Sequence 21, Appl	C 975	9.2	31.7	20	4	US-09-198-452A-2408	Sequence 2408, Ap
C 903	9.4	32.4	61	4	US-08-583-153A-21	Sequence 21, Appl	C 976	9.2	31.7	20	4	US-09-198-452A-3077	Sequence 3077, Ap

977 9.2 31.7 20 4 US-09-162-622-12 Sequence 12, Appl
978 9.2 31.7 20 4 US-09-509-015-12 Sequence 12, Appl
979 9.2 31.7 20 5 PCT-US95-06160-1 Sequence 1, Appl
980 9.2 31.7 20 5 PCT-US96-08235-12 Sequence 12, Appl
981 9.2 31.7 21 1 US-08-832-883-78 Sequence 78, Appl
982 9.2 31.7 21 2 US-08-832-877-78 Sequence 78, Appl
983 9.2 31.7 21 3 US-09-114-825-4 Sequence 4, Appl
984 9.2 31.7 21 3 US-09-114-825-5 Sequence 5, Appl
985 9.2 31.7 21 4 US-09-485-737B-50 Sequence 50, Appl
986 9.2 31.7 21 4 US-09-593-012-196 Sequence 196, App
987 9.2 31.7 21 4 US-09-422-978-6777 Sequence 6777, Ap
988 9.2 31.7 21 4 US-09-422-978-7947 Sequence 7947, Ap
989 9.2 31.7 21 4 US-09-422-978-10532 Sequence 10532, A
990 9.2 31.7 21 4 US-09-422-978-11518 Sequence 11518, A
991 9.2 31.7 22 2 US-09-044-506A-32 Sequence 32, Appl
992 9.2 31.7 22 2 US-09-336-946B-33 Sequence 33, Appl
993 9.2 31.7 22 4 US-08-975-902-44 Sequence 44, Appl
994 9.2 31.7 23 3 US-09-251-565-44 Sequence 44, Appl
995 9.2 31.7 23 3 US-09-254-733-14 Sequence 14, Appl
996 9.2 31.7 23 3 US-09-316-083-5 Sequence 5, Appl
997 9.2 31.7 23 4 US-09-533-700-5 Sequence 5, Appl
998 9.2 31.7 24 1 US-08-242-680-4 Sequence 4, Appl
999 9.2 31.7 24 2 US-08-464-257-5 Sequence 5, Appl
1000 9.2 31.7 24 2 US-08-653-382A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-956-171E-2762
; Sequence 2762, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2762:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2762:
US-08-956-171E-2762
Query Match 44.1%; Score 12.8; DB 4; Length 68;
Best Local Similarity 47.6%; Pred. No. 1.7e+02;
Matches 10; Conservative 4; Mismatches 7; Indels 0;
Gaps 0;
Qy 5 AUNCUTUNNGUAGCCCNANG 25
| : : : |||||
Db 3 ATCCTGTCTTAAGCCGACG 23
| : : : |||||
RESULT 2
5258283-10
; Patent No. 5258283
; APPLICANT: FRAZIER, MARVIN E.; MALLAVIA, LOUIS P.; SAMUEL,
; JAMES E.; BACA, OSWALD G.
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF COXIELLA
; BURNETII IN BIOLOGICAL FLUIDS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/425,856
; FILING DATE: 23-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 927,779
; FILING DATE: 05-NOV-1986
; APPLICATION NUMBER: 795,207
; FILING DATE: 05-NOV-1985
; SEQ ID NO:10:
; LENGTH: 27
5258283-10
Query Match 42.1%; Score 12.2; DB 6; Length 27;
Best Local Similarity 40.9%; Pred. No. 3.1e+02;
Matches 9; Conservative 5; Mismatches 8; Indels 0;
Gaps 0;
Qy 4 GAUNCUUNNGUAGCCCNANG 25
| : : : |||||
Db 4 GGTTCCTTGAATAAGCCCAATG 25
| : : : |||||
RESULT 3
US-08-410-654B-30
; Sequence 30, Application US/08410654B
; Patent No. 5833976
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin-10 to Treat
; TITLE OF INVENTION: Septic Shock
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,654B
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-410-854B-30

Query Match 42.1%; Score 12.2; DB 2; Length 69;
Best Local Similarity 43.5%; Pred. No. 3.8e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANGNG 27
| : : : : :
Db 11 ATGCCTTTAATAAGCTCCAAGAG 33

RESULT 4

US-08-474-851-30
Sequence 30, Application US/08474851
Patent No. 5837232
GENERAL INFORMATION:
APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,851
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-481-560-30

TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-474-851-30

Query Match 42.1%; Score 12.2; DB 2; Length 69;
Best Local Similarity 43.5%; Pred. No. 3.8e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANGNG 27
| : : : : :
Db 11 ATGCCTTTAATAAGCTCCAAGAG 33

RESULT 5

US-08-481-560-30
Sequence 30, Application US/08481560
Patent No. 5837293
GENERAL INFORMATION:
APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of Interleukin-10 to Modulate
TITLE OF INVENTION: Inflammation or T-Cell Mediated
TITLE OF INVENTION: Immune Function
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,560
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQ1GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-481-560-30


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; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IGT101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotide sequence encoding a streptavidin mimic
US-08-218-369-7

Query Match 40.0%; Score 11.6; DB 4; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
|||:::|::|::|::|::|
Db 31 GAAGCTTTAGGTGGGGCCCATGAG 8

RESULT 9
US-08-218-369-15
; Sequence 15, Application US/08218369
; Patent No. 6312699
; GENERAL INFORMATION:
; APPLICANT: Curriel, David T.
; APPLICANT: Engler, Jeffrey A.
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,369
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IGT101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotides 5 through 36 are complementary to nucl
US-08-218-369-15

Query Match 40.0%; Score 11.6; DB 4; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
|||:::|::|::|::|::|
Db 10 GAAGCTTTAGGTGGGGCCCATGAG 33

RESULT 10
US-09-904-599A-7/c
; Sequence 7, Application US/09904599A
; Patent No. 6683170
; GENERAL INFORMATION:
; APPLICANT: Curriel, David T.,
; APPLICANT: Engler, Jeffrey A.
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; FILE REFERENCE: D5839/D
; CURRENT APPLICATION NUMBER: US/09/904,599A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 08/218,369
; PRIOR FILING DATE: 1994-03-28
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 7
; LENGTH: 36
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence coding for streptavidin mimic
; OTHER INFORMATION: that binds biotin nucleotide sequence
US-09-904-599A-7

Query Match 40.0%; Score 11.6; DB 4; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
|||:::|::|::|::|::|
Db 31 GAAGCTTTAGGTGGGGCCCATGAG 8

RESULT 11
PCT-US95-03742-7/c
; Sequence 7, Application PC/TUS9503742
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03742
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IG1101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotide sequence
; OTHER INFORMATION: encoding a streptavidin mimic that binds biotin."
PCT-US95-03742-7

Query Match 40.0%; Score 11.6; DB 5; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAGCCCNANGNG 27
Db 31 GAAGCTTTAGTGGGGCCCATGAG 8

RESULT 12
PCT-US95-03742-15
; Sequence 15, Application PC/TUS9503742
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03742
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IG1101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature

```

```

; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotides 5 through 36
; OTHER INFORMATION: are complementary to nucleotides 5 through 36 of
; OTHER INFORMATION: Sequence ID No. 7."
PCT-US95-03742-15

Query Match 40.0%; Score 11.6; DB 5; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAGCCCNANGNG 27
Db 10 GAAGCTTTAGTGGGGCCCATGAG 33

RESULT 13
US-09-619-213B-45/c
; Sequence 45, Application US/09619213B
; Patent No. 6458539
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Smith, Jonathan Drew
; APPLICANT: Koch, Tad
; APPLICANT: Golden, Mace
; TITLE OF INVENTION: Photoselection of Nucleic Acid Ligands
; FILE REFERENCE: NEX10-5
; CURRENT APPLICATION NUMBER: US/09/619,213B
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/459,553
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 09/093,293
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 08/612,895
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: 08/123,935
; PRIOR FILING DATE: 1993-09-17
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: modified base
; LOCATION: (1)..(61)
; OTHER INFORMATION: All T's are 5-bromouracil
US-09-619-213B-45

Query Match 40.0%; Score 11.6; DB 4; Length 61;
Best Local Similarity 45.8%; Pred. No. 8.6e+02;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 4 GAUNCUUUNNGUAGCCCNANGNG 27
Db 42 GATACATATGACAGCCCATGAG 19

RESULT 14
US-09-849-069-37/c
; Sequence 37, Application US/09849069
; Patent No. 6630306
; GENERAL INFORMATION:
; APPLICANT: Ronald R. Breaker
; TITLE OF INVENTION: Bioreactive Allosteric Polynucleotides
; FILE REFERENCE: OCR-794.CIP
; CURRENT APPLICATION NUMBER: US/09/849,069
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/331,809
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: MS-DOS

```

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; SEQ ID NO 37
; LENGTH: 65
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA with 3 cleavage sites
US-09-849-069-37

Query Match      39.3%; Score 11.4; DB 4; Length 65;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      10 UUNNGUAGCCCNANGNG 27
DB      51 TTCGTAAGCCCATGAG 34

RESULT 15
US-08-741-881-28/c
; Sequence 28, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741.881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-28

Query Match      38.6%; Score 11.2; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      6 UUNCUUNGUAGCCCNANGNG 27
DB      24 TCCTTAGGTTAGCCGTACAAG 3

RESULT 16
US-08-739-158-28/c
; Sequence 28, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739.158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-28

Query Match      38.6%; Score 11.2; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      6 UUNCUUNGUAGCCCNANGNG 27
DB      24 TCCTTAGGTTAGCCGTACAAG 3

RESULT 17
US-08-739-167-28/c
; Sequence 28, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-28

Query Match 38.6%; Score 11.2; DB 2; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUUNNGUAGCCCNANGNG 27
Db 24 TCCTTTAGGTAGCCGTACAAG 3

RESULT 18
US-08-404-796-28/c
; Sequence 28, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-28

US-08-404-796-28

Query Match 38.6%; Score 11.2; DB 3; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUUNNGUAGCCCNANGNG 27
Db 24 TCCTTTAGGTAGCCGTACAAG 3

RESULT 19
US-08-931-869-28/c
; Sequence 28, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-28

Query Match 38.6%; Score 11.2; DB 3; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUUNNGUAGCCCNANGNG 27
Db 24 TCCTTTAGGTAGCCGTACAAG 3

RESULT 20
US-09-350-399-28/c
; Sequence 28, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-350-399-28
Query Match 38.6%; Score 11.2; DB 4; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 6 UCUUUNGUAGCCNANGNG 27
Db 24 TCCTTAGTTCGCGTACAAAG 3
RESULT 21
US-09-236-140A-28/c
Sequence 28, Application US/09236140A
Patent No. 6376236
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Ibanez, Carlos E.
Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Cullman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 823-6000
TELEFAX: (949) 823-6100
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-236-140A-28
Query Match 38.6%; Score 11.2; DB 4; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 6 UCUUUNGUAGCCNANGNG 27
Db 24 TCCTTAGTTCGCGTACAAAG 3
RESULT 22
US-08-741-881-29
Sequence 29, Application US/08741881
Patent No. 5789245
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Polo, John M.
Ibanez, Carlos E.
Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,881
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-741-881-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27
Db 6 TCCTTTAGGTAGCCGTACAG 27

RESULT 23

US-08-739-158-29
; Sequence 29, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-739-158-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27
Db 6 TCCTTTAGGTAGCCGTACAG 27

RESULT 24

US-08-739-167-29
; Sequence 29, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.

; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 2; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27
Db 6 TCCTTTAGGTAGCCGTACAG 27

RESULT 25

US-08-404-796-29
; Sequence 29, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W

APPLICANT: Polo, John M.

APPLICANT: Ibanez, Carlos E.

APPLICANT: Chang, Stephen M.W.

APPLICANT: Jolly, Douglas J.

APPLICANT: Driver, David A.

APPLICANT: Belli, Barbara A.

; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/404,796

FILING DATE: 15-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-29

Query Match 38.6%; Score 11.2; DB 3; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUNNGUAGCCCNANGNG 27
DB 6 TCCTTAGGTAGCGGTACAAG 27

RESULT 26
US-08-931-869-29
; Sequence 29, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-29

Query Match 38.6%; Score 11.2; DB 3; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;

Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 6 UNCUNNGUAGCCCNANGNG 27
DB 6 TCCTTAGGTAGCGGTACAAG 27

RESULT 27
US-09-350-399-29
; Sequence 29, Application US/09350399
; Patent No. 6342372
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,399
; FILING DATE: 08-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-09-350-399-29
Query Match 38.6%; Score 11.2; DB 4; Length 33;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUNNGUAGCCCNANGNG 27
DB 6 TCCTTAGGTAGCGGTACAAG 27

RESULT 28
US-09-236-140A-29
; Sequence 29, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES
; NUMBER OF SEQUENCES: 124

```
/
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
/ STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
/ CITY: NEWPORT BEACH
/ STATE: CALIFORNIA
/ COUNTRY: US
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA: US/09/235,140A
/ APPLICATION NUMBER: 39,645
/ FILING DATE: 22-Jan-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cullman, Louis C.
/ REGISTRATION NUMBER: 20263.332 / 1146.020
/ REFERENCE/DOCKET NUMBER:
/ TELEPHONE: (949) 823.6000
/ TELEFAX: (949) 823.6100
/
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 29:
/
/ US-09-236-140A-29
/
/ Query Match 38.6%; Score 11.2; DB 4; Length 33;
/ Best Local Similarity 36.4%; Pred. No. 1.3e+03;
/ Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 6 TCCTTTAGGTACCGTACAG 27
/
/ RESULT 29
/ US-08-642-045B-17/c
/ Sequence 17, Application US/08642045B
/ Patent No. 5851804
/ GENERAL INFORMATION:
/ APPLICANT: Snyder, Linda A.
/ APPLICANT: Satishchandran, C.
/ TITLE OF INVENTION: CHIMERIC KANAMYCIN RESISTANCE GENE
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5851804ris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19103
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect 6.0/5.1
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/642,045B
/ FILING DATE: 06-MAY-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: APOL-0262
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-642-045B-17
/
/ Query Match 38.6%; Score 11.2; DB 3; Length 36;
/ Best Local Similarity 40.9%; Pred. No. 1.3e+03;
/ Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 35 TCGTTCAGTTAAGACCGACGCG 14
/
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-642-045B-17
/
/ Query Match 38.6%; Score 11.2; DB 2; Length 36;
/ Best Local Similarity 40.9%; Pred. No. 1.3e+03;
/ Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 35 TCGTTCAGTTAAGACCGACGCG 14
/
/ RESULT 30
/ US-08-852-268-17/c
/ Sequence 17, Application US/08852268
/ Patent No. 6143527
/ GENERAL INFORMATION:
/ APPLICANT: Pachuk, Catherine J.
/ APPLICANT: Samuel, Manoj
/ APPLICANT: Zurawski, John A.
/ APPLICANT: Satishchandran, C.
/ TITLE OF INVENTION: CHAIN REACTION CLONING
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6143527ris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19103
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/852,268
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/642,045
/ FILING DATE: 06-MAY-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: APOL-0265
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-852-268-17
/
/ Query Match 38.6%; Score 11.2; DB 3; Length 36;
/ Best Local Similarity 40.9%; Pred. No. 1.3e+03;
/ Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 35 TCGTTCAGTTAAGACCGACGCG 14
```

```
RESULT 31
US-09-571-774-2
; Sequence 2, Application US/09571774
; Patent No. 6479262
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; TITLE OF INVENTION: Solid Phase Enzymatic Assembly of Polynucleotides
; FILE REFERENCE: HER-0005
; CURRENT APPLICATION NUMBER: US/09/571,774
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Oligonucleotide
US-09-571-774-2

Query Match      38.6%; Score 11.2; DB 4; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
||| : : : |||||
Db      16 GATTCCTCTGTTAGCCCA 35

RESULT 32
US-09-852-385-2
; Sequence 2, Application US/09852385
; Patent No. 6635453
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Marrs, Barry
; TITLE OF INVENTION: Methods For The Enzymatic Assembly Of Polynucleotides And Identif
; TITLE OF INVENTION: Of Polynucleotides Having Desired Characteristics
; FILE REFERENCE: HER-0042
; CURRENT APPLICATION NUMBER: US/09/852,385
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/571,774
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6635453el Sequence
US-09-852-385-2

Query Match      38.6%; Score 11.2; DB 4; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
||| : : : |||||
Db      16 GATTCCTCTGTTAGCCCA 35

RESULT 33
US-09-422-978-2842
; Sequence 2842, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
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; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2842
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-19348-229 : polymorphic base T or C
US-09-422-978-2842

Query Match      38.6%; Score 11.2; DB 4; Length 47;
Best Local Similarity 55.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
||| : : : |||||
Db      16 GAATCTATYAGCAGCCCTA 35

RESULT 34
US-09-310-463-6
; Sequence 6, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: DNA
; ORGANISM: human
US-09-310-463-6

Query Match      38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy      6 UNCUCUUNNGUAGCCCNANG 27
||| : : : |||||
Db      27 TTCCTCTATAACCCCGAGTG 48

RESULT 35
US-08-842-248A-6
; Sequence 6, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
```

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 36
US-09-364-380-29
; Sequence 29, Application US/09364380A
; Patent No. 6171795
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Nucleic Acid Ligands to CD40Ligand
; FILE REFERENCE: NEX85
; CURRENT APPLICATION NUMBER: US/09/364,380A
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 70
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)..(70)
; OTHER INFORMATION: All pyrimidines are 2' F.
US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 3; Length 70;
Best Local Similarity 61.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Query Match 38.6%; Score 11.2; DB 3; Length 70;
Best Local Similarity 61.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 3; Length 70;
Best Local Similarity 61.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 3; Length 70;
Best Local Similarity 61.9%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

US-09-364-380-29

US-08-323-531-71/c
; Sequence 71, Application US/08323531
; Patent No. 5731189
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesvirus
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/926,784
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide primer
US-08-323-531-71

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-323-531-71

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-323-531-71

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-323-531-71

US-08-842-248A-6

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-08-842-248A-6

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-08-842-248A-6

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-08-842-248A-6

US-08-198-094-71/c
; Sequence 71, Application US/08198094
; Patent No. 5741696
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesvirus
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

US-09-364-380-29

US-08-198-094-71/c
; Sequence 71, Application US/08198094
; Patent No. 5741696
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesvirus
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

US-08-198-094-71/c

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,094
FILING DATE: February 17, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Synthetic oligonucleotide primer
US-08-198-094-71

Query Match 37.9%; Score 11; DB 1; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18
|:|::|:|
Db 20 ATACTTTCGTAAG 7

RESULT 39
US-08-480-640A-119/c
Sequence 119 Application US/08480640A
Patent No. 603934
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Equine Influenza A neuraminidase
STRAIN: Prague/56
US-08-480-640A-119

Query Match 37.9%; Score 11; DB 3; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18
|:|::|:|
Db 20 ATACTTTCGTAAG 7

RESULT 40
US-08-295-802-119/c
Sequence 119 Application US/08295802
Patent No. 6127163
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 188
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,802
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Equine Influenza A neuraminidase
STRAIN: Prague/56
US-08-295-802-119

Query Match 37.9%; Score 11; DB 3; Length 31;
Best Local Similarity 42.9%; Pred. No. 1.7e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18
|:|::|:|
Db 20 ATACTTTCGTAAG 7

Search completed: April 18, 2004, 09:59:45
Job time : 50.6667 secs